

# SEQUENCE LISTING

<110> Falco, Saverio Carl  
Hitz, William D.  
Kinney, Anthony J.  
Cahoon, Rebecca E.  
Rafalski, J. Antoni

<120> PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES

<130> BB-1126

<140>

<141>

<150> 60/063,423

<151> 1997 October 28

<160> 54

<170> Microsoft Word Version 7.0A

<210> 1

<211> 2135

<212> DNA

<213> Zea mays

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 Glu Leu Lys Leu Asn Lys Tyr Ser Ala Arg Ile Thr Glu Pro Lys Ser  
 35 40 45  
 Gln Gly Ala Ser Gln Ala Val Leu Tyr Gly Val Gly Leu Thr Asp Ala  
 50 55 60  
 Asp Leu Arg Lys Pro Gln Val Gly Val Ser Ser Val Trp Tyr Glu Gly  
 65 70 75 80  
 Asn Thr Cys Asn Met His Leu Leu Arg Leu Ala Glu Ala Val Arg Asp  
 85 90 95  
 Gly Val Arg Glu Ala Gly Met Val Gly Phe Arg Phe Asn Thr Val Gly  
 100 105 110  
 Val Ser Asp Ala Ile Ser Met Gly Thr Arg Gly Met Cys Tyr Ser Leu  
 115 120 125  
 Gln Ser Arg Asp Leu Ile Ala Asp Ser Ile Glu Thr Val Met Gly Ala  
 130 135 140  
 Gln His Tyr Asp Ala Asn Ile Ser Ile Pro Gly Cys Asp Lys Asn Met  
 145 150 155 160  
 Pro Gly Thr Ile Met Ala Met Gly Arg Leu Asn Arg Pro Ser Ile Met  
 165 170 175  
 Ile Tyr Gly Gly Thr Ile Lys Pro Gly His Phe Gln Gly Asn Ser Tyr  
 180 185 190  
 Asp Ile Val Ser Ala Phe Gln Cys Tyr Gly Glu Tyr Val Ser Gly Ser  
 195 200 205  
 Ile Thr Asp Glu Gln Arg Lys Asn Val Leu Arg Asn Ser Cys Pro Gly  
 210 215 220  
 Ala Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ala Ser Ala  
 225 230 235 240  
 Ile Glu Thr Leu Gly Met Ser Leu Pro Tyr Ser Ser Ser Thr Pro Ala  
 245 250 255  
 Glu Asp Pro Leu Lys Leu Glu Glu Cys Arg Leu Ala Gly Lys Tyr Leu  
 260 265 270  
 Leu Glu Leu Leu Lys Met Asp Leu Lys Pro Lys Asp Ile Ile Thr Glu  
 275 280 285  
 Lys Ser Leu Arg Asn Ala Met Val Ile Val Met Ala Leu Gly Gly Ser  
 290 295 300  
 Thr Asn Ala Val Leu His Leu Ile Ala Ile Ala Arg Ser Val Gly Leu  
 305 310 315 320

His Leu Thr Leu Asp Asp Phe Gln Lys Val Ser Asp Gln Val Pro Phe  
325 330 335

Leu Ala Asp Leu Lys Pro Ser Gly Lys Tyr Val Met Glu Asp Leu His  
340 345 350

Lys Ile Gly Gly Thr Pro Ala Val Ile His Tyr Leu Leu Glu Gln Gly  
355 360 365

Leu Leu Asp Gly Asp Cys Met Thr Val Thr Gly Lys Thr Leu Ala Glu  
370 375 380

Asn Ala Lys Ile Phe Pro Pro Leu Ser Glu Gly Gln Gln Ile Ile Arg  
385 390 395 400

Pro Leu Asp Asn Pro Ile Lys Pro Thr Gly His Ile Gln Ile Leu Tyr  
405 410 415

Gly Asn Leu Ala Pro Glu Gly Ser Val Ala Lys Ile Thr Gly Lys Glu  
420 425 430

Gly Leu Phe Phe Ser Gly Pro Ala Leu Val Phe Glu Gly Glu Glu Ser  
435 440 445

Met Ile Thr Ala Ile Ser Glu Asn Pro Ala Asn Phe Lys Gly Lys Val  
450 455 460

Val Val Ile Arg Gly Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu  
465 470 475 480

Met Leu Thr Pro Thr Ser Ala Ile Met Gly Ala Gly Leu Gly Lys Glu  
485 490 495

Cys Ala Leu Leu Thr Asp Gly Arg Phe Ser Gly Gly Ser His Gly Phe  
500 505 510

Val Val Gly His Ile Cys Pro Glu Ala Gln Glu Gly Gly Pro Ile Gly  
515 520 525

Leu Val His Ser Gly Asp Val Ile Thr Ile Asp Val Ser Lys Arg Val  
530 535 540

Ile Asp Val Asp Leu Thr Glu Gln Gln Leu Glu Glu Arg Arg Arg Lys  
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Trp Thr Pro Pro Pro Tyr Lys Ser Thr Cys Gly Ala Leu Trp Lys Tyr  
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<212> DNA  
<213> Glycine max

<400> 3  
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aattctggtc atgttctct ctccgttgc gctccatcg ccgtggaac cccacggag 180  
acggtgaagc tgaacaagta cagctccgc atcaccgagc ccaaatcgca gggcgctcc 240  
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gocgtgogtg acggcgttgc tgctgctggc atggttccct tccgcttcaa caccgttggc 420  
gtcagcgaag ccattctccat gggcaccgt ggcattgtgt acagcctcca gtccagggac 480  
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100374501-100374501

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Lys Pro Gly His Phe Glu Gly Asn Thr Phe Asp Ile Val Ser Ala Phe	195	200	205
Gln Cys Tyr Gly Glu Tyr Val Ser Gly Ser Ile Asn Asp Asp Gln Arg	210	215	220
Gln Asn Val Ile Arg Asn Ser Cys Pro Gly Ala Gly Ala Cys Gly Gly	225	230	235
Met Tyr Thr Ala Asn Thr Met Ala Ser Ala Ile Glu Ala Met Gly Met	245	250	255
Ser Leu Pro Tyr Ser Ser Ser Thr Pro Ala Glu Asp Pro Leu Lys Leu	260	265	270
Asp Glu Cys Arg Leu Ala Gly Lys Tyr Leu Leu Glu Leu Leu Lys Met	275	280	285
Asp Leu Lys Pro Arg Asp Ile Ile Thr Arg Lys Ser Leu Arg Asn Ala	290	295	300
Met Val Ile Val Met Ala Leu Gly Gly Ser Thr Asn Ala Val Leu His	305	310	315
Leu Ile Ala Ile Ala Lys Ser Val Gly Ile Asp Leu Thr Leu Asp Asp	325	330	335
Phe Gln Lys Val Ser Asp Glu Val Pro Phe Ile Ala Asp Leu Lys Pro	340	345	350
Ser Gly Lys Tyr Val Met Glu Asp Val His Lys Ile Gly Gly Thr Pro	355	360	365
Ala Val Ile Arg Tyr Leu Leu Glu Gln Gly Phe Leu Asp Gly Asp Cys	370	375	380
Met Thr Val Thr Gly Lys Thr Leu Ala Glu Asn Ala Glu Leu Val Pro	385	390	395
Pro Leu Ser Asn Gly Gln Glu Ile Ile Arg Pro Val Glu Asn Pro Ile	405	410	415
Lys Lys Thr Ala His Ile Gln Ile Leu Tyr Gly Asn Leu Ala Pro Gln	420	425	430
Gly Ser Val Ala Lys Ile Thr Gly Lys Glu Gly Leu Tyr Phe Ser Gly	435	440	445
Pro Ala Leu Val Phe Glu Gly Glu Glu Ala Met Ile Ala Ala Ile Ser	450	455	460
Glu Asp Pro Ser Ser Phe Lys Gly Lys Val Val Val Ile Arg Gly Glu	465	470	475
Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu Thr Pro Thr Ser	485	490	495
Ala Ile Met Gly Ala Gly Leu Gly Lys Glu Val Ala Leu Leu Thr Asp	500	505	510
Gly Arg Phe Ser Gly Gly Ser His Gly Phe Val Val Gly His Ile Cys	515	520	525

Pro Glu Ala Gln Glu Gly Gly Pro Ile Gly Leu Ile Gln Asn Gly Asp  
 530 535 540

Val Ile Asn Val Asp Ile Lys Asn Arg Arg Ile Asp Val Leu Val Ser  
 545 550 555 560

Asp Glu Glu Met Glu Ala Arg Arg Lys Lys Trp Thr Ala Pro Pro Tyr  
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Lys Ala Asn Arg Gly Ala Leu Tyr Lys Tyr Ile Lys Asn Val Thr Pro  
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Ala Ser Ser Gly Cys Val Thr Asp Glu  
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 <212> DNA  
 <213> Triticum aestivum

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 <221> unsure  
 <222> (447)

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 tttcaaggga aaggtttag tgatccgagg agaaggacca aaaggagggtc ccgggatgcc 180  
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 tgaagcacag gaaggaggcc caattggtct tgttgagaat ggcgatacaa tcacgatcga 360  
 cgtcgggaag aaagtaattg atgttgattt gacggaagac cagcttgaac aaaggcgaag 420  
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 <213> Triticum aestivum

<220>  
 <221> UNSURE  
 <222> (149)

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Phe Ser Gly Pro Ala Leu Val Phe Asp Gly Glu Glu Ser Met Ile Thr  
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Ala Ile Ser Glu Asn Pro Ala Asn Phe Lys Gly Lys Val Val Val Ile  
 35 40 45

Arg Gly Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu Thr  
 50 55 60

Pro Thr Ser Ala Ile Met Gly Ala Gly Leu Gly Lys Glu Cys Ala Leu  
 65 70 75 80

Leu Thr Asp Gly Arg Phe Ser Gly Gly Ser His Gly Phe Val Val Gly  
 85 90 95

His Val Cys Pro Glu Ala Gln Glu Gly Gly Pro Ile Gly Leu Val Glu  
 100 105 110

Asn	Gly	Asp	Thr	Ile	Thr	Ile	Asp	Val	Gly	Lys	Lys	Val	Ile	Asp	Val
		115					120					125			
Asp	Leu	Thr	Glu	Asp	Gln	Leu	Glu	Gln	Arg	Arg	Arg	Lys	Trp	Ser	Pro
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<211>	585														
<212>	PRT														
<213>	Saccharomyces cerevisiae														
<400>	7														
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Pro	Lys	Gly	Gln	Gly	Ala	Ser	Gln	Ala	Met	Leu	Tyr	Ala	Thr	Gly	Phe
		35					40					45			
Lys	Lys	Glu	Asp	Phe	Lys	Lys	Pro	Gln	Val	Gly	Val	Gly	Ser	Cys	Trp
	50					55					60				
Trp	Ser	Gly	Asn	Pro	Cys	Asn	Met	His	Leu	Leu	Asp	Leu	Asn	Asn	Arg
65					70					75					80
Cys	Ser	Gln	Ser	Ile	Glu	Lys	Ala	Gly	Leu	Lys	Ala	Met	Gln	Phe	Asn
				85					90					95	
Thr	Ile	Gly	Val	Ser	Asp	Gly	Ile	Ser	Met	Gly	Thr	Lys	Gly	Met	Arg
			100					105					110		
Tyr	Ser	Leu	Gln	Ser	Arg	Glu	Ile	Ile	Ala	Asp	Ser	Phe	Glu	Thr	Ile
		115					120					125			
Met	Met	Ala	Gln	His	Tyr	Asp	Ala	Asn	Ile	Ala	Ile	Pro	Ser	Cys	Asp
	130					135					140				
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145					150					155					160
Ser	Ile	Met	Val	Tyr	Gly	Gly	Thr	Ile	Leu	Pro	Gly	His	Pro	Thr	Cys
				165					170					175	
Gly	Ser	Ser	Lys	Ile	Ser	Lys	Asn	Ile	Asp	Ile	Val	Ser	Ala	Phe	Gln
			180					185					190		
Ser	Tyr	Gly	Glu	Tyr	Ile	Ser	Lys	Gln	Phe	Thr	Glu	Glu	Glu	Arg	Glu
		195					200					205			
Asp	Val	Val	Glu	His	Ala	Cys	Pro	Gly	Pro	Gly	Ser	Cys	Gly	Gly	Met
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225					230					235					240
Ile	Pro	Asn	Ser	Ser	Ser	Phe	Pro	Ala	Val	Ser	Lys	Glu	Lys	Leu	Ala
				245					250					255	
Glu	Cys	Asp	Asn	Ile	Gly	Glu	Tyr	Ile	Lys	Lys	Thr	Met	Glu	Leu	Gly
			260					265					270		

Ile Leu Pro Arg Asp Ile Leu Thr Lys Glu Ala Phe Glu Asn Ala Ile  
275 280 285

Thr Tyr Val Val Ala Thr Gly Gly Ser Thr Asn Ala Val Leu His Leu  
290 295 300

Val Ala Val Ala His Ser Ala Gly Val Lys Leu Ser Pro Asp Asp Phe  
305 310 315 320

Gln Arg Ile Ser Asp Thr Thr Pro Leu Ile Gly Asp Phe Lys Pro Ser  
325 330 335

Gly Lys Tyr Val Met Ala Asp Leu Ile Asn Val Gly Gly Thr Gln Ser  
340 345 350

Val Ile Lys Tyr Leu Tyr Glu Asn Asn Met Leu His Gly Asn Thr Met  
355 360 365

Thr Val Thr Gly Asp Thr Leu Ala Glu Arg Ala Lys Lys Ala Pro Ser  
370 375 380

Leu Pro Glu Gly Gln Glu Ile Ile Lys Pro Leu Ser His Pro Ile Lys  
385 390 395 400

Ala Asn Gly His Leu Gln Ile Leu Tyr Gly Ser Leu Ala Pro Gly Gly  
405 410 415

Ala Val Gly Lys Ile Thr Gly Lys Glu Gly Thr Tyr Phe Lys Gly Arg  
420 425 430

Ala Arg Val Phe Glu Glu Glu Gly Ala Phe Ile Glu Ala Leu Glu Arg  
435 440 445

Gly Glu Ile Lys Lys Gly Glu Lys Thr Val Val Val Ile Arg Tyr Glu  
450 455 460

Gly Pro Arg Gly Ala Pro Gly Met Pro Glu Met Leu Lys Pro Ser Ser  
465 470 475 480

Ala Leu Met Gly Tyr Gly Leu Gly Lys Asp Val Ala Leu Leu Thr Asp  
485 490 495

Gly Arg Phe Ser Gly Gly Ser His Gly Phe Leu Ile Gly His Ile Val  
500 505 510

Pro Glu Ala Ala Glu Gly Gly Pro Ile Gly Leu Val Arg Asp Gly Asp  
515 520 525

Glu Ile Ile Ile Asp Ala Asp Asn Asn Lys Ile Asp Leu Leu Val Ser  
530 535 540

Asp Lys Glu Met Ala Gln Arg Lys Gln Ser Trp Val Ala Pro Pro Pro  
545 550 555 560

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565 570 575

Ala Ser Asn Gly Cys Val Leu Asp Ala  
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<212> DNA  
<213> Zea mays





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 <212> PRT  
 <213> Zea mays

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 Arg Ala Ser Pro Gly Gly Thr Gly Gly Val Lys Thr Ile Gly Asn Tyr  
 35 40 45  
 Ala Ser Val Leu Lys Ala Gln Lys Ile Ala Lys Gly Lys Gly Tyr Ser  
 50 55 60  
 Asp Val Leu Tyr Leu Asp Ala Val His Asp Lys Tyr Leu Glu Glu Val  
 65 70 75 80  
 Ser Ser Cys Asn Ile Phe Val Val Lys Asp Asn Val Ile Ser Thr Pro  
 85 90 95  
 Ala Ile Lys Gly Thr Ile Leu Pro Gly Ile Thr Arg Lys Ser Ile Ile  
 100 105 110  
 Glu Val Ala Gln Ser Lys Gly Phe Lys Val Glu Glu Arg Leu Val Cys  
 115 120 125  
 Val Asp Glu Leu Ile Asn Ala Asp Glu Val Phe Cys Thr Gly Thr Ala  
 130 135 140  
 Val Val Val Ser Pro Val Gly Ser Val Thr Tyr Met Gly Lys Arg Val  
 145 150 155 160  
 Glu Tyr Gly Asn Gln Gly Val Gly Val Val Ser Gln Gln Leu Tyr Lys  
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gtttccatcg acgatctggt ggccgcagac gaggtgttct gcaccgggac cgcggtggtg 180  
gttgctcccg tgtcgacagt cacgtaccag ggcgagaggt atgagttcag aacggggccg 240  
gacacggtgt cncaggagct gtacacgacg ctgacatcca ttcagatggg catggccgcc 300  
gaggacagca ngggatggac agtaccagta gagtanatta ataaggttgg ggaatncatc 360  
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<212> PRT  
<213> Zea mays

<220>  
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<220>  
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Gly Tyr Lys Val Glu Glu Arg Leu Val Ser Ile Asp Asp Leu Val Ala  
35 40 45

Ala Asp Glu Val Phe Cys Thr Gly Thr Ala Val Val Val Ala Pro Val  
50 55 60  
Ser Thr Val Thr Tyr Gln Gly Glu Arg Tyr Glu Phe Arg Thr Gly Pro  
65 70 75 80  
Asp Thr Val Ser Gln Glu Leu Tyr Thr Thr Leu Thr Ser Ile Gln Met  
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Gly Met Ala Ala Glu Asp Ser Xaa Gly Trp Thr Val Pro Val Glu Xaa  
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Ile Asn Lys  
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<212> DNA  
<213> Oryza sativa

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catgtgcatg ccgtcgccgt cgggtggagca gttcgtccac gccgtcaagc agaccgtcct 240  
cgccaaccgc cgctgggtgc caccgcaagg aaagggggcg ctgtacatca ggccgctgct 300  
catcgggagc ggaccgattc tcgggctggc tcccgccccg gactacacgt tcctcatcta 360  
cgccgcaccg gttggaacgt acttcaagga ggggtctagcg ccgataaacc ttgtcgtaga 420  
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caagagcgtc atcgagctcg ccagggaccg cggctatcag gttgaagaac ggctcgtctc 720  
catcgacgat ctggtcggcg cagacgaggt gttctgcacc ggaacagcg tggtcgttgc 780  
cccagtatcg agtggtactt accatgggca aaggtacgag ttcaggactg gacatgacac 840  
gttatcgtag acactgcaca cgactctgac gtccatccag atgggcctgg ctgaggacaa 900  
gaaaggatgg acagtggcaa tagattaagg atggattatg ggcaaaggga tcccgattat 960  
tcctcatgtc atccaatgta gattattgtc gttttatata tcttcctgta gcgacagtga 1020  
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<212> PRT  
<213> Oryza sativa

<400> 15  
Glu Gly Ile Leu Ser Arg Tyr Gly Asn Ile Glu Leu Ser Pro Ser Ser  
1 5 10 15  
Gly Val Ile Asn Tyr Gly Gln Gly Leu Phe Glu Gly Leu Lys Ala Tyr  
20 25 30  
Arg Ala Ala Asn Gln Gln Gly Ser Tyr Met Leu Phe Arg Pro Glu Glu  
35 40 45  
Asn Ala Arg Arg Met Gln His Gly Ala Glu Arg Met Cys Met Pro Ser  
50 55 60  
Pro Ser Val Glu Gln Phe Val His Ala Val Lys Gln Thr Val Leu Ala  
65 70 75 80  
Asn Arg Arg Trp Val Pro Pro Gln Gly Lys Gly Ala Leu Tyr Ile Arg  
85 90 95

Pro Leu Leu Ile Gly Ser Gly Pro Ile Leu Gly Leu Ala Pro Ala Pro  
100 105 110

Glu Tyr Thr Phe Leu Ile Tyr Ala Ala Pro Val Gly Thr Tyr Phe Lys  
115 120 125

Glu Gly Leu Ala Pro Ile Asn Leu Val Val Glu Asp Ser Ile His Arg  
130 135 140

Ala Met Pro Gly Gly Thr Gly Gly Val Lys Thr Ile Thr Asn Tyr Ala  
145 150 155 160

Pro Val Leu Lys Ala Gln Met Asp Ala Lys Ser Ile Gly Phe Thr Asp  
165 170 175

Val Leu Tyr Leu Asp Ala Val His Lys Thr Tyr Leu Glu Glu Ala Ser  
180 185 190

Ser Cys Asn Leu Phe Ile Val Lys Asp Gly Val Val Ala Thr Pro Ala  
195 200 205

Thr Val Gly Thr Ile Leu Pro Gly Ile Thr Arg Lys Ser Val Ile Glu  
210 215 220

Leu Ala Arg Asp Arg Gly Tyr Gln Val Glu Glu Arg Leu Val Ser Ile  
225 230 235 240

Asp Asp Leu Val Gly Ala Asp Glu Val Phe Cys Thr Gly Thr Ala Val  
245 250 255

Val Val Ala Pro Val Ser Ser Val Thr Tyr His Gly Gln Arg Tyr Glu  
260 265 270

Phe Arg Thr Gly His Asp Thr Leu Ser Gln Thr Leu His Thr Thr Leu  
275 280 285

Thr Ser Ile Gln Met Gly Leu Ala Glu Asp Lys Lys Gly Trp Thr Val  
290 295 300

Ala Ile Asp  
305

<210> 16  
<211> 965  
<212> DNA  
<213> Glycine max

<400> 16  
catccttggt tgtccatgct cccgagttgt gaatatcagg gactgcctca gctcctocat 60  
tgactttcct tggagttgta agcccagctt agaagaggct acgctgatgt ccattttcta 120  
aagtttaatt tcaactccca atatcacaag tttatataga tatatgcttt tttgaaagag 180  
gctcgtgcgc aattcggcac gaggaatg gagagcattc gactaattta cccgatctgc 240  
ccctctagac attcttctt tcttctctct catcaatctc ccttctctatg cgaaccttct 300  
ctctctctca agcttcgaaa gcagtttctt ctcaacttgc agaatgttct ggaagccgco 360  
tctcctctca ggccttcgc cactctgtct tctgatccct acagtgcagac gattgaatta 420  
gctgatatag aatgggacaa ccttgggttt gggcttcaac ccactgatta tatgtatata 480  
atgaaatgca cacgaggtgg aaccttttcc aaaggtgaat tgcagcgttt tgggaacata 540  
gagttgaacc cctccgctgg agtttttaaac tatggccagg gattatttga gggtttgaaa 600  
gcataacgca aacaagatgg gagtatactc ctcttccgtc cggaagaaaa tggtttgagg 660  
atgcagatag gtgcggagcg gatgtgcatg ccatcaccta ctatggagca gtttgggaa 720  
gctgtgaagg atactgttt agctaacaaa cggtgggttc cccctgcagg taaagggttc 780  
ttgtatatta gacctttgtt aatgggaagt ggacctgtac ttggtgttgc acctgcacca 840  
gagtacacat ttctaataata tgtttcacct gttgggaact acttcaagga aggtttggcc 900  
ccaatcaatt tgattgtaga aaatgaattc catcgtgcaa ctctggtgg cactggagct 960  
cgtgc 965

<210> 17  
 <211> 252  
 <212> PRT  
 <213> Glycine max

<400> 17

Met Glu Ser Ile Arg Leu Ile Tyr Pro Ile Cys Pro Ser Arg His Ser  
 1 5 10 15  
 Ser Phe Leu Leu Ser His Gln Ser Pro Phe Leu Cys Glu Pro Ser Leu  
 20 25 30  
 Ser Leu Lys Leu Arg Lys Gln Phe Pro Leu Thr Ser Gln Asn Val Leu  
 35 40 45  
 Glu Ala Ala Ser Pro Leu Arg Pro Ser Ala Thr Leu Ser Ser Asp Pro  
 50 55 60  
 Tyr Ser Glu Thr Ile Glu Leu Ala Asp Ile Glu Trp Asp Asn Leu Gly  
 65 70 75 80  
 Phe Gly Leu Gln Pro Thr Asp Tyr Met Tyr Ile Met Lys Cys Thr Arg  
 85 90 95  
 Gly Gly Thr Phe Ser Lys Gly Glu Leu Gln Arg Phe Gly Asn Ile Glu  
 100 105 110  
 Leu Asn Pro Ser Ala Gly Val Leu Asn Tyr Gly Gln Gly Leu Phe Glu  
 115 120 125  
 Gly Leu Lys Ala Tyr Arg Lys Gln Asp Gly Ser Ile Leu Leu Phe Arg  
 130 135 140  
 Pro Glu Glu Asn Gly Leu Arg Met Gln Ile Gly Ala Glu Arg Met Cys  
 145 150 155 160  
 Met Pro Ser Pro Thr Met Glu Gln Phe Val Glu Ala Val Lys Asp Thr  
 165 170 175  
 Val Leu Ala Asn Lys Arg Trp Val Pro Pro Ala Gly Lys Gly Ser Leu  
 180 185 190  
 Tyr Ile Arg Pro Leu Leu Met Gly Ser Gly Pro Val Leu Gly Val Ala  
 195 200 205  
 Pro Ala Pro Glu Tyr Thr Phe Leu Ile Tyr Val Ser Pro Val Gly Asn  
 210 215 220  
 Tyr Phe Lys Glu Gly Leu Ala Pro Ile Asn Leu Ile Val Glu Asn Glu  
 225 230 235 240  
 Phe His Arg Ala Thr Pro Gly Gly Thr Gly Ala Arg  
 245 250

<210> 18  
 <211> 1501  
 <212> DNA  
 <213> Triticum aestivum

<400> 18

gcacgagccg cgcggcacgt cgggtctccc cagcccccagg ccgcacccgg gcctaccctc 60  
 gcaacccatt cagaagcgat tgtccggcag cgcgcgtctcc gtctccaggc gaggcactgc 120  
 ggcaaggagc agcccggtgt cgcgccctgat gacggcatca tacaacacag gaactccgga 180  
 cctagtcgac ttgcactggg agactcttgg atttcaactg gtcccgcagg actttatgta 240  
 tataatgaaa tggtcgtcag atgggggtgt caccaagggt gaattgggtc catatggggc 300  
 aatcgagctg aacctgctg ctgcagtttt aaattatggc cagggtattg tcgaaggctc 360

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tagagcacac agaaaggagg atggttcagt agttgttttt cgccccaagg aaaacgcggt 420
gcggtatgagg ataggtgcag atcggctatg catgcctgoa ccaagcggtg agcagttcct 480
atcagctgtc aagcacacta tattggcaaa caagcggttg gtacccccca ctggcaaagg 540
ttctttatat atcaggccgc tgcgtattgg aagtggagct atgctaggtg tagcacctgc 600
cccgaggtat acatttggtg tgtatgtttg ccagttggt cactatttca aggatggcct 660
gtcaccaatt agcttattga ctgaggaaga atatcacgcg gctgcacctg gtggaactgg 720
tgatattaag acaattggaa attatgcttc ggttgttagt gctcagagaa gagccaagga 780
gaaaggtoat tctgatgttc tttacttgga tcccgtgcat aagaagtttg tggaggaagt 840
ttcttcctgt aatatattga tgggtgaagga taatgttatt tctactccac tattaacggg 900
aacaattcct cctggaatca caagaagaag tataattgaa attgcccata atcttggaa 960
ccaggtcgaa gagcgctta ttgcgataga tgagttgctt gacgctgatg aagtcttctg 1020
tacagggact gccgtgtac tatcacccgt tggttccatt gtgtaccacg gaagaagagt 1080
ggagtatggg ggcgggaagg tccgagcggg gtcccagcaa ctgtattcgg cacttacagc 1140
tatccagaaa ggccttggtg aggacagtat gggatggagt gtgcagttga attagcagct 1200
tcatcatctg gacggtctct acgagcctcc tccgcaagaa aacaatgcaa aatcacttga 1260
ccctctgtca ggaattttg cagaatgtag aatagcataa tttccctgtg aagatagcaa 1320
gaggtacaca cacaacatag catcaagctg gatcagaaa attaataata atgattaaat 1380
agctgttgtt tcttctcatt ctgtttccca agaggactga atgcgctttg agtgtgaata 1440
actccataac atacttgcaa ttgcaaacca tgagacataa ataattggtg gcaaaaaaaaa 1500
a 1501

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<210> 19
<211> 348
<212> PRT
<213> Triticum aestivum

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<400> 19
Met Thr Ala Ser Tyr Asn Thr Gly Thr Pro Asp Leu Val Asp Phe Asp
 1          5          10          15

Trp Glu Thr Leu Gly Phe Gln Leu Val Pro Thr Asp Phe Met Tyr Ile
 20          25          30

Met Lys Cys Ser Ser Asp Gly Val Phe Thr Lys Gly Glu Leu Val Pro
 35          40          45

Tyr Gly Pro Ile Glu Leu Asn Pro Ala Ala Ala Val Leu Asn Tyr Gly
 50          55          60

Gln Gly Leu Leu Glu Gly Leu Arg Ala His Arg Lys Glu Asp Gly Ser
 65          70          75          80

Val Val Val Phe Arg Pro Lys Glu Asn Ala Leu Arg Met Arg Ile Gly
 85          90          95

Ala Asp Arg Leu Cys Met Pro Ala Pro Ser Val Glu Gln Phe Leu Ser
100          105          110

Ala Val Lys His Thr Ile Leu Ala Asn Lys Arg Trp Val Pro Pro Thr
115          120          125

Gly Lys Gly Ser Leu Tyr Ile Arg Pro Leu Leu Ile Gly Ser Gly Ala
130          135          140

Met Leu Gly Val Ala Pro Ala Pro Glu Tyr Thr Phe Val Val Tyr Val
145          150          155          160

Cys Pro Val Gly His Tyr Phe Lys Asp Gly Leu Ser Pro Ile Ser Leu
165          170          175

Leu Thr Glu Glu Glu Tyr His Arg Ala Ala Pro Gly Gly Thr Gly Asp
180          185          190

Ile Lys Thr Ile Gly Asn Tyr Ala Ser Val Val Ser Ala Gln Arg Arg
195          200          205

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Ala Lys Glu Lys Gly His Ser Asp Val Leu Tyr Leu Asp Pro Val His  
 210 215 220

Lys Lys Phe Val Glu Glu Val Ser Ser Cys Asn Ile Leu Met Val Lys  
 225 230 235 240

Asp Asn Val Ile Ser Thr Pro Leu Leu Thr Gly Thr Ile Leu Pro Gly  
 245 250 255

Ile Thr Arg Arg Ser Ile Ile Glu Ile Ala Gln Asn Leu Gly Ile Gln  
 260 265 270

Val Glu Glu Arg Leu Ile Ala Ile Asp Glu Leu Leu Asp Ala Asp Glu  
 275 280 285

Val Phe Cys Thr Gly Thr Ala Val Val Leu Ser Pro Val Gly Ser Ile  
 290 295 300

Val Tyr His Gly Arg Arg Val Glu Tyr Gly Gly Gly Lys Val Gly Ala  
 305 310 315 320

Val Ser Gln Gln Leu Tyr Ser Ala Leu Thr Ala Ile Gln Lys Gly Leu  
 325 330 335

Val Glu Asp Ser Met Gly Trp Ser Val Gln Leu Asn  
 340 345

<210> 20  
 <211> 363  
 <212> PRT  
 <213> Bacillus subtilis

<400> 20  
 Met Thr Lys Gln Thr Ile Arg Val Glu Leu Thr Ser Thr Lys Lys Pro  
 1 5 10 15

Lys Pro Asp Pro Asn Gln Leu Ser Phe Gly Arg Val Phe Thr Asp His  
 20 25 30

Met Phe Val Met Asp Tyr Ala Ala Asp Lys Gly Trp Tyr Asp Pro Arg  
 35 40 45

Ile Ile Pro Tyr Gln Pro Leu Ser Met Asp Pro Thr Ala Met Val Tyr  
 50 55 60

His Tyr Gly Gln Thr Val Phe Glu Gly Leu Lys Ala Tyr Val Ser Glu  
 65 70 75 80

Asp Asp His Val Leu Leu Phe Arg Pro Glu Lys Asn Met Glu Arg Leu  
 85 90 95

Asn Gln Ser Asn Asp Arg Leu Cys Ile Pro Gln Ile Asp Glu Glu Gln  
 100 105 110

Val Leu Glu Gly Leu Lys Gln Leu Val Ala Ile Asp Lys Asp Trp Ile  
 115 120 125

Pro Asn Ala Glu Gly Thr Ser Leu Tyr Ile Arg Pro Phe Ile Ile Ala  
 130 135 140

Thr Glu Pro Phe Leu Gly Val Ala Ala Ser His Thr Tyr Lys Leu Leu  
 145 150 155 160

Ile Ile Leu Ser Pro Val Gly Ser Tyr Tyr Lys Glu Gly Ile Lys Pro  
 165 170 175





<212> PRT  
<213> Glycine max

<400> 22

Ala Arg Val Gln Pro Lys Ala Arg Ile Gly Thr Pro Phe Pro Arg Asp  
1 5 10 15  
Thr Leu Arg Ser Ile Leu Val Gln Met Thr Ala Ala Ser Asn Cys Arg  
20 25 30  
Arg Gly Ser Ile Arg Tyr Trp Leu Ser Ala Gly Gly Gly Asp Phe Leu  
35 40 45  
Leu Ser Ser Ala Gly Cys Ala Gly Pro Ala Phe Tyr Ala Val Val Ile  
50 55 60  
Pro Thr Asp Tyr Ser Gln Cys Arg His Gly Val Arg Ala Val Thr Thr  
65 70 75 80  
Ser Val Pro Met Lys Pro Pro Leu Phe Ala Thr Met Lys Asn Val Asn  
85 90 95  
Tyr Leu Pro Asn Val Leu Ser Ile Met Asp Ala Glu Asp Arg Gly Ala  
100 105 110  
Phe Ala Ser Val Trp Val Asp Gly Glu Gly Asn Val Ala Glu Gly Pro  
115 120 125  
Met Val Asn Val Ala Phe Val Thr Ala Ala Gly Glu Leu Val Leu Pro  
130 135 140  
Ala Phe Asp Lys Ile Leu Ala Gly Cys Thr Ala Lys Arg Leu Leu Ala  
145 150 155 160  
Leu Ala Pro Arg Leu Val Glu Ser Gly Leu Leu Lys Ala Val Thr Thr  
165 170 175  
Arg His Ile Ala Ala Asp Glu Ala Lys Arg Cys Ser Ala Glu Met Ala  
180 185 190  
Phe Val Gly Ser Gly Leu Pro Val Leu Pro Ile Val Glu Trp Asp Asp  
195 200 205  
Gln Leu Ile Gly Asp Gly Lys Val Gly Lys Thr Met Met Ala Leu Ser  
210 215 220  
Asp Leu Leu Trp Glu Asp Met Lys Ser Gly Pro Asp Arg Ile Ala Val  
225 230 235 240

Pro Tyr Lys

<210> 23  
<211> 1045  
<212> DNA  
<213> Glycine max

<400> 23

gcacgaggct atggttattc ctatggatga ccacatggtc cacagaggcc acggtgtctt 60  
tgatactgca gcaataatgg atggataoct atatgagcta gatcaacacc ttgatcgctt 120  
tttaagggtca gcatccatgt ctaaaataga tccccattt gatcgaggaa gcataagaag 180  
aatactcata caaactgtaa gtgcttccaa gtgtagaaaa ggatcactaa gatattggct 240  
ctcggcagga cctggcgact ttcagttatc tccctcttgt tgccaccgat caagtctgta 300  
tcgcatagta atacaggatc tgtcaccatc ctcacctaatt ttcaggggcg ttaaagtgt 360  
cacttcatct attcccatta aacaccccaa gtttgctatc actaagagtg tgaactatct 420  
tccaaatgtg ctctcaaagg tggaagotga agaagctggt gctttttagt gcatttggct 480

tgatggtgaa ggttttgttg ctgaagggcc taatatgaat gtggcctttg tcaactaaaga 540  
 taaggaactt ataatgccac actttgacaa aattctaagt ggctgcacag ctaagagagt 600  
 ttttaaccctt gctgagagct tgtaagga gggtaagctt aaagggataa gggtgaaaac 660  
 tgtgactgtc gaggaaggta agcaagcaga tgaaatgatg cttcttggca gcggagttct 720  
 tgtttgccct gtagtgcaat gggatgagca gggtattggg gatggcaaag aaggccctat 780  
 aacgcaggct ctcttaaatc taattgttga ggacatgaaa tcaggtcctt ccactgttcg 840  
 tatacctggt ccttattgac acaactttat ttcttctctt tcattttgta atgaagatta 900  
 atcagtagtt gtgatgcccc tacttctaca gggaggaatg actattaata acttcattgt 960  
 ctaatgggtt ttagagcttg tagtggtata agaaactcta ttccatggag cttagttttc 1020  
 aaatgttttt gtggtctaaa aaaaa 1045

<210> 24  
 <211> 285  
 <212> PRT  
 <213> Glycine max

<400> 24  
 His Glu Ala Met Val Ile Pro Met Asp Asp His Met Val His Arg Gly  
 1 5 10 15  
 His Gly Val Phe Asp Thr Ala Ala Ile Met Asp Gly Tyr Leu Tyr Glu  
 20 25 30  
 Leu Asp Gln His Leu Asp Arg Phe Leu Arg Ser Ala Ser Met Ser Lys  
 35 40 45  
 Ile Asp Pro Pro Phe Asp Arg Gly Ser Ile Arg Arg Ile Leu Ile Gln  
 50 55 50  
 Thr Val Ser Ala Ser Lys Cys Arg Lys Gly Ser Leu Arg Tyr Trp Leu  
 65 70 75 80  
 Ser Ala Gly Pro Gly Asp Phe Gln Leu Ser Pro Ser Cys Cys His Arg  
 85 90 95  
 Ser Ser Leu Tyr Ala Ile Val Ile Gln Asp Leu Ser Pro Ser Ser Pro  
 100 105 110  
 Asn Phe Arg Gly Val Lys Val Val Thr Ser Ser Ile Pro Ile Lys His  
 115 120 125  
 Pro Lys Phe Ala Ile Thr Lys Ser Val Asn Tyr Leu Pro Asn Val Leu  
 130 135 140  
 Ser Lys Val Glu Ala Glu Glu Ala Gly Ala Phe Val Gly Ile Trp Leu  
 145 150 155 160  
 Asp Gly Glu Gly Phe Val Ala Glu Gly Pro Asn Met Asn Val Ala Phe  
 165 170 175  
 Val Thr Lys Asp Lys Glu Leu Ile Met Pro His Phe Asp Lys Ile Leu  
 180 185 190  
 Ser Gly Cys Thr Ala Lys Arg Val Leu Thr Leu Ala Glu Ser Leu Leu  
 195 200 205  
 Arg Glu Gly Lys Leu Lys Gly Ile Arg Val Lys Thr Val Thr Val Glu  
 210 215 220  
 Glu Gly Lys Gln Ala Asp Glu Met Met Leu Leu Gly Ser Gly Val Leu  
 225 230 235 240  
 Val Cys Pro Val Val Gln Trp Asp Glu Gln Val Ile Gly Asp Gly Lys  
 245 250 255

Glu Gly Pro Ile Thr Gln Ala Leu Leu Asn Leu Ile Val Glu Asp Met  
 260 265 270

Lys Ser Gly Pro Ser Thr Val Arg Ile Pro Val Pro Tyr  
 275 280 285

<210> 25  
 <211> 1323  
 <212> DNA  
 <213> Oryza sativa

<400> 25  
 gcacgagagg aacccccactc acaaggtcccc tgaggttgaa aatgatgggtg atttttaaagt 60  
 tcatctgttc tcttcatcat ccgagttgct tgaaaagctt catgaaaaat ggagttcagt 120  
 ggagaaacca ccatacccag ctatgtattc tagtatttat ggaggtatca tacttgatcc 180  
 agcaatgatg gtaatcccca ttgatgatca catggttcac agagggcagtg gtgtgtttga 240  
 tacagctatt gttctagatg gatacctcta tgagttggat gttcaccttg acagattcct 300  
 aagttcagcc tccaaagcaa agatatcctc tcccttttct cgatcagtgcc ttcacagcat 360  
 tctaatacaa ctaactgcag catcaaaatg caagaaggga actctaagat actggctcag 420  
 tgcaggtcct ggagatttct tgctatcatc agcaggatgt ccaacatctg cattctatgc 480  
 agtagtcatt gaccaagatg tttcccaatg caaagaggga gttaaagtga ttacttccaa 540  
 cataccaatg aagccttctc tatttgccac agccaaaaat gtgaactatc ttccaaatgt 600  
 cctttcagta atggaagctg aagagaaagg agcatcttct tctatatggg ttgatgagga 660  
 aggttatatt gctgaaggctc caaatgtgaa tgttgctttc ataactcaag acaaggaaact 720  
 tgtcatgcct ccttttgata acatottaca tggttgcact gcaaaaaggc tccttgaact 780  
 ggcacccaag ttggttgatc aagggttctt gaaaggtgta gcaactaaaa aactaactgt 840  
 ggaggaagct aaagctgctg ctgaaatgat gtatgttaga agcacgcttc ctctgttgcc 900  
 tatcatcgct tgggatgac aaccatttg caacggaagg gtgggagaat taacaatggt 960  
 actttcggat atgctttggg atgatatggt agctggccct ggcacacaga ggatacctgt 1020  
 tccttatgtt gagtaaacct acaaagtcac caaattacag gctgggaaca actttcttac 1080  
 ttttctatgt catgttccta ggagttctcc ttgcaaagat ttatcaagag gtttctcttt 1140  
 gtatttgctt tttgtatttc aagtgtgaac actgaacaag tcctaaaagt aagcaccagg 1200  
 tgtttcctgc aacgcaaaat ttaogtagca gataaatagt ccttgaactg tttcacgctg 1260  
 ttgtattgat ataataataa taatgaagac ctttcatgct gctttgtgcc tgaaaaaaa 1320  
 aaa 1323

<210> 26  
 <211> 297  
 <212> PRT  
 <213> Oryza sativa

<400> 26  
 Met Tyr Ser Ser Ile Tyr Gly Gly Ile Ile Leu Asp Pro Ala Met Met  
 1 5 10 15  
 Val Ile Pro Ile Asp Asp His Met Val His Arg Gly His Gly Val Phe  
 20 25 30  
 Asp Thr Ala Ile Val Leu Asp Gly Tyr Leu Tyr Glu Leu Asp Val His  
 35 40 45  
 Leu Asp Arg Phe Leu Ser Ser Ala Ser Lys Ala Lys Ile Ser Ser Pro  
 50 55 60  
 Phe Ser Arg Ser Val Leu His Ser Ile Leu Ile Gln Leu Thr Ala Ala  
 65 70 75 80  
 Ser Lys Cys Lys Lys Gly Thr Leu Arg Tyr Trp Leu Ser Ala Gly Pro  
 85 90 95  
 Gly Asp Phe Leu Leu Ser Ser Ala Gly Cys Pro Thr Ser Ala Phe Tyr  
 100 105 110  
 Ala Val Val Ile Asp Gln Asp Val Ser Gln Cys Lys Glu Gly Val Lys  
 115 120 125

Val Ile Thr Ser Asn Ile Pro Met Lys Pro Ser Leu Phe Ala Thr Ala  
130 135 140

Lys Asn Val Asn Tyr Leu Pro Asn Val Leu Ser Val Met Glu Ala Glu  
145 150 155 160

Glu Lys Gly Ala Ser Ser Ser Ile Trp Val Asp Glu Glu Gly Tyr Ile  
165 170 175

Ala Glu Gly Pro Asn Val Asn Val Ala Phe Ile Thr Gln Asp Lys Glu  
180 185 190

Leu Val Met Pro Pro Phe Asp Asn Ile Leu His Gly Cys Thr Ala Lys  
195 200 205

Arg Leu Leu Glu Leu Ala Pro Lys Leu Val Asp Gln Gly Leu Leu Lys  
210 215 220

Gly Val Ala Thr Lys Lys Leu Thr Val Glu Glu Ala Lys Ala Ala Ala  
225 230 235 240

Glu Met Met Tyr Val Gly Ser Thr Leu Pro Leu Leu Pro Ile Ile Val  
245 250 255

Trp Asp Asp Gln Pro Ile Gly Asn Gly Arg Val Gly Glu Leu Thr Met  
260 265 270

Leu Leu Ser Asp Met Leu Trp Asp Asp Met Val Ala Gly Pro Gly Thr  
275 280 285

Gln Arg Ile Pro Val Pro Tyr Val Glu  
290 295

<210> 27  
<211> 542  
<212> DNA  
<213> Triticum aestivum

<400> 27  
gcacgaggtt atcttcatct ggctgtacaa acccagccct ctatgctggt gttattgaaa 60  
gccatcctt acaagtaccg tcctgctgca gagggtcac atcatctata ccgataaagt 120  
ctcctcaatt tgcagtcattg aaaagcgtga attacttgc caatgcactc accaaggttg 180  
aaggagaaga gaatggtgca tttactggca tttggctaga cgatgagggc ttcgttgag 240  
aggggttcgaa catgaatggt ggcttcgtga caaagaacaa ggagcttctc atgcctcgtt 300  
ttgacaagat cctgagtggg tgcacagcaa gacgggttct gaccctcgct gagcatctag 360  
tagctcatgg aaagctcagc agggtaatat caaggaatgt gagtgttgag gaagggaaga 420  
tggcogatga gatgatgctc atcggtagt gcatcttctg caaacctgtt gttcagtgagg 480  
atgataagat aattggttct ggacaagaag gcccgatagc tcaagcgtag tatgacataa 540  
tt 542

<210> 28  
<211> 180  
<212> PRT  
<213> Triticum aestivum

<400> 28  
Thr Arg Leu Ser Ser Ser Gly Cys Thr Asn Pro Ala Leu Tyr Ala Val  
1 5 10 15

Val Ile Glu Ser Pro Ser Leu Gln Val Pro Ser Cys Cys Arg Val Val  
20 25 30

Thr Ser Ser Ile Pro Ile Lys Ser Pro Gln Phe Ala Val Met Lys Ser  
35 40 45

Val Asn Tyr Leu Pro Asn Ala Leu Thr Lys Val Glu Gly Glu Glu Asn  
50 55 60

Gly Ala Phe Thr Gly Ile Trp Leu Asp Asp Glu Gly Phe Val Ala Glu  
65 70 75 80

Gly Ser Asn Met Asn Val Gly Phe Val Thr Lys Asn Lys Glu Leu Leu  
85 90 95

Met Pro Arg Phe Asp Lys Ile Leu Ser Gly Cys Thr Ala Arg Arg Val  
100 105 110

Leu Thr Leu Ala Glu His Leu Val Ala His Gly Lys Leu Ser Arg Val  
115 120 125

Ile Ser Arg Asn Val Ser Val Glu Glu Gly Lys Met Ala Asp Glu Met  
130 135 140

Met Leu Ile Gly Ser Gly Ile Leu Val Lys Pro Val Val Gln Trp Asp  
145 150 155 160

Asp Lys Ile Ile Gly Ser Gly Gln Glu Gly Pro Ile Ala Gln Ala Leu  
165 170 175

Tyr Asp Leu Ile  
180

<210> 29  
<211> 288  
<212> PRT  
<213> Methanococcus jannaschii

<400> 29

Met Lys Ile Tyr Leu Asn Gly Lys Phe Val Asp Glu Lys Asp Ala Lys  
1 5 10 15

Val Ser Val Phe Asp His Gly Leu Leu Tyr Gly Asp Gly Val Phe Glu  
20 25 30

Gly Ile Arg Ala Tyr Asp Gly Val Val Phe Met Leu Lys Glu His Ile  
35 40 45

Asp Arg Leu Tyr Asp Ser Ala Lys Ser Leu Cys Ile Asp Ile Pro Leu  
50 55 60

Thr Lys Glu Glu Met Ile Asp Val Val Leu Glu Thr Leu Arg Val Asn  
65 70 75 80

Asn Leu Arg Asp Ala Tyr Ile Arg Leu Val Val Thr Arg Gly Val Gly  
85 90 95

Asp Leu Gly Leu Asp Pro Arg Lys Cys Gly Lys Pro Thr Ile Phe Cys  
100 105 110

Ile Ala Ile Pro Met Pro Pro Leu Leu Gly Glu Asp Gly Ile Arg Ala  
115 120 125

Ile Thr Val Ser Val Arg Arg Leu Pro Val Asp Val Leu Asn Pro Ala  
130 135 140

Val Lys Ser Leu Asn Tyr Leu Asn Ser Val Leu Ala Lys Ile Gln Ala  
145 150 155 160

Asn Tyr Ala Gly Val Asp Glu Ala Phe Leu Leu Asp Asp Lys Gly Phe  
165 170 175

Val Val Glu Gly Thr Gly Asp Asn Ile Phe Ile Val Lys Asn Gly Val  
180 185 190

Leu Lys Thr Pro Pro Val Tyr Gln Ser Ile Leu Lys Gly Ile Thr Arg  
195 200 205

Asp Val Val Ile Lys Leu Ala Lys Glu Glu Gly Ile Glu Val Val Glu  
210 215 220

Glu Pro Leu Thr Leu His Asp Leu Tyr Thr Ala Asp Glu Leu Phe Ile  
225 230 235 240

Thr Gly Thr Ala Ala Glu Ile Val Pro Val Phe Glu Ile Asp Gly Arg  
245 250 255

Val Ile Asn Asn Lys Gln Val Gly Glu Ile Thr Lys Lys Leu Lys Glu  
260 265 270

Lys Phe Lys Asp Ile Arg Thr Lys Trp Gly Ile Lys Val Tyr Asp Glu  
275 280 285

<210> 30  
<211> 1062  
<212> DNA  
<213> Zea mays

<400> 30  
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acaaggagga gatgctgttt gggaagggtt acgtatatat gatggaaaag tattcaaatt 180  
agatgaacat ttggacagat tgtttgattc tgcaaaagct atggccttca gcaatgtgcc 240  
tactcgtgat tggattaagg atgccatctt taagactctg attgcaaatt gaatgttcaa 300  
caatgctcat ataaggctca cgctcacccg tgggaaaaag gtgacatctg gaatgagtcc 360  
agctttcaat ctttatgggt gtgccttgat tgtgcttgca gagtggaaac caccagttta 420  
tgataactct catgggataa aattggttac tgccaccaca cgtcgaaatt ctccaaatag 480  
tatagatccc aagattcatc acaacaatct tatcaacaat attctggcaa agatagaagg 540  
taatcttgcc caggctgagg atgccattat gctagataag gatggctttg tatcagaaac 600  
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gttacatgaa cgacgcatta caccggttgt aatgattgat ggacgtgaaa tcggcgacgg 780  
cggaacaatg ggtgaaatca caccggttgt aatgattgat ggacgtgaaa tcggcgacgg 840  
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<210> 31  
<211> 310  
<212> PRT  
<213> Zea mays

<400> 31  
Gln Pro Pro Leu Ser Asp Pro Pro Leu Pro Val Pro Ala Asn Lys Asn  
1 5 10 15

Ile Leu Val Trp Val Gly Asp Glu Leu Leu Pro Arg Asn Ser Ala Lys  
20 25 30

Val Ser Val Phe Asp Ser Val Val Gln Gly Gly Asp Ala Val Trp Glu  
35 40 45

Gly Leu Arg Ile Tyr Asp Gly Lys Val Phe Lys Leu Asp Glu His Leu  
50 55 60

Asp Arg Leu Phe Asp Ser Ala Lys Ala Met Ala Phe Ser Asn Val Pro  
65 70 75 80

Thr Arg Asp Trp Ile Lys Asp Ala Ile Phe Lys Thr Leu Ile Ala Asn  
 85 90 95  
 Gly Met Phe Asn Asn Ala His Ile Arg Leu Thr Leu Thr Arg Gly Lys  
 100 105 110  
 Lys Val Thr Ser Gly Met Ser Pro Ala Phe Asn Leu Tyr Gly Cys Ala  
 115 120 125  
 Leu Ile Val Leu Ala Glu Trp Lys Pro Pro Val Tyr Asp Asn Ser His  
 130 135 140  
 Gly Ile Lys Leu Val Thr Ala Thr Thr Arg Arg Asn Ser Pro Asn Ser  
 145 150 155 160  
 Ile Asp Pro Lys Ile His His Asn Asn Leu Ile Asn Asn Ile Leu Ala  
 165 170 175  
 Lys Ile Glu Gly Asn Leu Ala Gln Ala Glu Asp Ala Ile Met Leu Asp  
 180 185 190  
 Lys Asp Gly Phe Val Ser Glu Thr Asn Ala Thr Asn Ile Phe Met Val  
 195 200 205  
 Lys Lys Gly Ile Val Leu Thr Pro His Ala Asp Tyr Cys Leu Pro Gly  
 210 215 220  
 Ile Thr Arg Ala Thr Val Met Asp Leu Val Val Lys Glu Asn Phe Val  
 225 230 235 240  
 Leu His Glu Arg Arg Ile Ser Leu Ser Glu Phe His Ala Ala Asp Glu  
 245 250 255  
 Val Trp Thr Thr Gly Thr Met Gly Glu Ile Thr Pro Val Val Met Ile  
 260 265 270  
 Asp Gly Arg Glu Ile Gly Asp Gly Lys Ile Gly Pro Val Thr Arg Gln  
 275 280 285  
 Ile Gln Lys Ala Tyr Lys Ile Leu Thr Ala Gly Gln Gly Val Pro Ile  
 290 295 300  
 Pro Gly Val Ala Glu Val  
 305 310

<210> 32  
 <211> 1186  
 <212> DNA  
 <213> *Triticum aestivum*

<400> 32  
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 aatgggatgt tcaataatgc acatataagg ctcaactctca cccgtgggaa gaaggtagca 180  
 tctggaatga gtccaacttt caatctatat ggggtgtgtct tgattgtact tgcagagtgg 240  
 aaaccaccag tttatgataa ctcacatggg ataaagtgg taactgccgc cacacgtcgt 300  
 aattctccaa atagcgtaga ttccaagata catcacaaca atcttattaa caacattctg 360  
 gcaaagatag aaggtaatct tgcacaggct gaggatgcta tcatgctaga tcaagatggg 420  
 tttgtatcag aaacaaatgc aacaaacata tttatggtta agaagggcat tgtattgaca 480  
 cctcatgagg actactgcct tccaggaatt acccgtgcaa ctgtcaagga tcttgttgtg 540  
 aaagaaaacc tggattatca tgaacggcga attagtctat ctgaatttca tgctgcagat 600  
 gaggtgtgga caaccggaac aatgggtgaa attacaccgg ttgtgatgat tgacgggctg 660  
 gaaattggtg atgggaaaat cgggtctggtc acaagacaaa tccagagcgc atacaaagtc 720  
 ctgacagcag ggttgggagt aacaattccc aggaatgcgg aggcataatc atttgccgag 780  
 acattcttct tgtccttttg aaaaggagaa ggcacctatt atctatggac aaactttcag 840



gggttcagttt cgagtaatga taataaatac ccctccatcc ggaattactt gtcgtagaaa 900  
 tgggtaaaaa tgaatgtatc tagaactaaa aatacgttta gatacatcta tttctccgac 960  
 aggtatttcc ggatggaggg agtagtagct agcgttcaaa gaagcaccca gtgaaagtgg 1020  
 cacaccggac agaaaactga gtattcgaaa aatactggct gggctctgtga attcatgatt 1080  
 tactgtgtgc ctgtgtgctc cgaacctgtg gctgatcctg gacacagaac agaaaataga 1140  
 atattatatg cggttttatt ttctgctaaa aaaaaaaaaa aaaaaa 1186

<210> 33  
 <211> 255  
 <212> PRT  
 <213> Triticum aestivum

<400> 33  
 Ala Arg Val Lys Leu Glu Glu His Leu Asp Arg Leu Phe Asp Ser Thr  
 1 5 10 15  
 Lys Ala Met Ala Phe Ser Asn Val Pro Ser Arg Asp Trp Ile Lys Asp  
 20 25 30  
 Ala Ile Phe Lys Thr Leu Asn Ala Asn Gly Met Phe Asn Asn Ala His  
 35 40 45  
 Ile Arg Leu Thr Leu Thr Arg Gly Lys Lys Val Thr Ser Gly Met Ser  
 50 55 60  
 Pro Thr Phe Asn Leu Tyr Gly Cys Val Leu Ile Val Leu Ala Glu Trp  
 65 70 75 80  
 Lys Pro Pro Val Tyr Asp Asn Ser His Gly Ile Lys Leu Val Thr Ala  
 85 90 95  
 Ala Thr Arg Arg Asn Ser Pro Asn Ser Val Asp Ser Lys Ile His His  
 100 105 110  
 Asn Asn Leu Ile Asn Asn Ile Leu Ala Lys Ile Glu Gly Asn Leu Ala  
 115 120 125  
 Gln Ala Glu Asp Ala Ile Met Leu Asp Gln Asp Gly Phe Val Ser Glu  
 130 135 140  
 Thr Asn Ala Thr Asn Ile Phe Met Val Lys Lys Gly Ile Val Leu Thr  
 145 150 155 160  
 Pro His Ala Asp Tyr Cys Leu Pro Gly Ile Thr Arg Ala Thr Val Lys  
 165 170 175  
 Asp Leu Val Val Lys Glu Asn Leu Val Leu His Glu Arg Arg Ile Ser  
 180 185 190  
 Leu Ser Glu Phe His Ala Ala Asp Glu Val Trp Thr Thr Gly Thr Met  
 195 200 205  
 Gly Glu Ile Thr Pro Val Val Met Ile Asp Gly Arg Glu Ile Gly Asp  
 210 215 220  
 Gly Lys Ile Gly Leu Val Thr Arg Gln Ile Gln Ser Ala Tyr Lys Val  
 225 230 235 240  
 Leu Thr Ala Gly Leu Gly Val Thr Ile Pro Arg Asn Ala Glu Ala  
 245 250 255

<210> 34  
 <211> 210  
 <212> PRT  
 <213> Escherichia coli

<400> 34  
Met Thr Thr Lys Lys Ala Asp Tyr Trp Asn Gly Met Val Arg Trp Asp  
1 5 10 15  
Ala Lys Val His Val Met Ser His Ala His Tyr Gly Thr Ser Val Gly  
20 25 30  
Arg Cys Tyr Asp Ser His Lys Gly Val Val Arg His Arg His Met Arg  
35 40 45  
His Asp Ser Ala Lys Tyr Arg Val Ser Ser Asp Met Ala Cys Arg Asp  
50 55 60  
Val Arg Lys Asn Asn Thr Ser Ala Tyr Arg Val Gly Asp Val Gly Met  
65 70 75 80  
Gly Val Asn Ala Gly Tyr Ser Thr Asp Val Ala Ala Trp Gly Ala Tyr  
85 90 95  
Gly Ala Ala Gly Asp Ala Met Val Ser Ser Trp Asn Arg Ala Ala Asn  
100 105 110  
Thr Thr Ala Ala Lys Ala Gly Gly Asn Tyr Ser Ser Val Gly Ser Ala  
115 120 125  
Arg Arg His Gly Tyr Gly Ala Asp Val Asn Gly Tyr Ser Gly Ala Gly  
130 135 140  
Asn Val Lys Asp Gly Val Thr Thr Ser Ser Ala Gly Thr Arg Asp Ala  
145 150 155 160  
Lys Ala Lys Gly Val Arg Val Ser Arg Ser Tyr Ala Asp Val Met Ser  
165 170 175  
Gly Thr Ala Ala Thr Val Arg Ser Val Asp Gly Val Gly Gly Arg Cys  
180 185 190  
Gly Val Thr Lys Arg Ala Gly Thr Gly Thr Asp Lys Trp Gly Trp Asp  
195 200 205  
Val Asn  
210

<210> 35  
<211> 1626  
<212> DNA  
<213> Zea mays

<400> 35  
gcacgagagc ccgggggagaa cgtgtgggtg gacatcgacg tgctcatgac gcacgacgtc 60  
tgccgggcccgc gcaccatcgg catcttcaag aaggagttcg gggaggatgc caaggtctgg 120  
gaccgcgaga aggtcgatcat catccccgac cactacatct tcaccagcga cgagcgcgcc 180  
aaccgcaacg tcgatatacct cagggaacttc tgtctggagc agaacatcaa gtacttctat 240  
gatatcaagg acctcagcga tttcagggtc aatccagact acaagggtgt ctgccacatt 300  
gcacttgctc aggaaggcca ctgccgacca gccgaggttc tcttggttac tgattctcat 360  
acgtgcaatg ctggagcctt tgggtcaattt gcaaccggaa ttggaaacac tgatgcaggt 420  
tttgtgatgg gcaactggaaa ggctcttctc aagggtgccac ctactatcag gtttgtatta 480  
gatggagaaa tgccgcctta tttacttgcg aaggatctga ttttgcaaat tattggtgag 540  
atttcagtat ctggtgcaac ctacaaatcg atggagtttg ttggatcaac tgtagaaagt 600  
ctaaccatgg aagaacgtat gacactatgc aacatgggtg ttgaagctgg tggaaagaac 660  
ggtgtcgtgc ctgctgatga aactacattt aaataccttg aggttaggac atcagttgat 720  
tatcaacctg tctacagtga tgctgaggcc agatttttta gtgactaccg gtttgatgta 780  
tcgaaactgg agccagtagt tgccaagcca cattgcctg acaaccgtgc cctagcaaga 840  
gaatgcaaag atgtcaagat cgaccgagtc tatattggtt cctgcactgg tggcaagact 900  
gaggacttcc ttgctgcccgc aaaggtgttc ttagcctcgg gaaagaaggt taaagttccc 960  
acattccttg tccctgcccac acaaaaggtg tggatggacg tatatagcct tcctgtacca 1020

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ggatctggcg gcaaaacttg cgcccagata ttcgaggagg ctggttgtga tacaccagca 1080
agtcctaatt gcggcgcttg tctgggtggc cctcgcgata cgatatgcacg gatgaatgaa 1140
cctacgggtct gcgtgtccac cacgaacagg aacttcccgg gcaggatggg gcacaaggaa 1200
gggcagatct acctggcgtc cccctacacc gctgcagcct cgccctgac ggggtacgtc 1260
acggacccca gggacttcct catgtgaacg atcttgaaac agccacagag tgcctgcacc 1320
gctgtttttt gtgttgaacc ttagtttagg cgtgtgccct tcgttgagaa ataaactccc 1380
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cgataacgta gttgagcgtt acaagggaaa tacattcatt ctttccagta tcgatggcag 1500
tcactagact ccgttcttac aaaaaaaagg catgtcgaga gatctttagg ttcatacact 1560
tgttaaaaca cttttttgta caatgtatgg gaaagaagct cagtcgaaaa aaaaaaaaaa 1620
aaaaaa

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<210> 36
<211> 428
<212> PRT
<213> Zea mays

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<400> 36
Ala Arg Glu Pro Gly Glu Asn Val Trp Val Asp Ile Asp Val Leu Met
 1          5          10          15

Thr His Asp Val Cys Gly Pro Gly Thr Ile Gly Ile Phe Lys Lys Glu
 20          25          30

Phe Gly Glu Asp Ala Lys Val Trp Asp Arg Glu Lys Val Val Ile Ile
 35          40          45

Pro Asp His Tyr Ile Phe Thr Ser Asp Glu Arg Ala Asn Arg Asn Val
 50          55          60

Asp Ile Leu Arg Asp Phe Cys Leu Glu Gln Asn Ile Lys Tyr Phe Tyr
 65          70          75          80

Asp Ile Lys Asp Leu Ser Asp Phe Arg Ala Asn Pro Asp Tyr Lys Gly
 85          90          95

Val Cys His Ile Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly Glu
100          105          110

Val Leu Leu Gly Thr Asp Ser His Thr Cys Asn Ala Gly Ala Phe Gly
115          120          125

Gln Phe Ala Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Met Gly
130          135          140

Thr Gly Lys Ala Leu Leu Lys Val Pro Pro Thr Ile Arg Phe Val Leu
145          150          155          160

Asp Gly Glu Met Pro Pro Tyr Leu Leu Ala Lys Asp Leu Ile Leu Gln
165          170          175

Ile Ile Gly Glu Ile Ser Val Ser Gly Ala Thr Tyr Lys Ser Met Glu
180          185          190

Phe Val Gly Ser Thr Val Glu Ser Leu Thr Met Glu Glu Arg Met Thr
195          200          205

Leu Cys Asn Met Val Val Glu Ala Gly Gly Lys Asn Gly Val Val Pro
210          215          220

Ala Asp Glu Thr Thr Phe Lys Tyr Leu Glu Gly Arg Thr Ser Val Asp
225          230          235          240

Tyr Gln Pro Val Tyr Ser Asp Ala Glu Ala Arg Phe Phe Ser Asp Tyr
245          250          255

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Arg Phe Asp Val Ser Lys Leu Glu Pro Val Val Ala Lys Pro His Ser  
 260 265 270  
 Pro Asp Asn Arg Ala Leu Ala Arg Glu Cys Lys Asp Val Lys Ile Asp  
 275 280 285  
 Arg Val Tyr Ile Gly Ser Cys Thr Gly Gly Lys Thr Glu Asp Phe Leu  
 290 295 300  
 Ala Ala Ala Lys Val Phe Leu Ala Ser Gly Lys Lys Val Lys Val Pro  
 305 310 315 320  
 Thr Phe Leu Val Pro Ala Thr Gln Lys Val Trp Met Asp Val Tyr Ser  
 325 330 335  
 Leu Pro Val Pro Gly Ser Gly Gly Lys Thr Cys Ala Gln Ile Phe Glu  
 340 345 350  
 Glu Ala Gly Cys Asp Thr Pro Ala Ser Pro Asn Cys Gly Ala Cys Leu  
 355 360 365  
 Gly Gly Pro Arg Asp Thr Tyr Ala Arg Met Asn Glu Pro Thr Val Cys  
 370 375 380  
 Val Ser Thr Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His Lys Glu  
 385 390 395 400  
 Gly Gln Ile Tyr Leu Ala Ser Pro Tyr Thr Ala Ala Ala Ser Ala Leu  
 405 410 415  
 Thr Gly Tyr Val Thr Asp Pro Arg Asp Phe Leu Met  
 420 425

<210> 37  
 <211> 1688  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> unsure  
 <222> (1673)

<400> 37  
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 cgccgcgcgc ccctcaegac atggcctcct ccgtctccgc cgccgccaaag gccgcgcgcg 120  
 cggttcgcga caaggtccag aaggagctgg ccgcgcgcgc gcagcgccgc gcgggcttga 180  
 cccgcgcggac caagccgtgc agcgtgcgcg ccgtcgcttc gccgcgcgcg gccctgtcgt 240  
 ccaccggctc ggtgaagagc gcgatgacga tgacggagaa gatactggcg cgggcgctcg 300  
 agcgcgcgcg gctggagccc ggggagaacg tgtgggtcga cgtcgacgtg ctcatgacgc 360  
 acgacgtctg cgggcccggc gccttcgaca tcttcaagaa ggagttcggg gaggacgcca 420  
 ggggtctggga ccgcgagaag ctctgtctca tcccggaacca ctacatcttc accagcgacg 480  
 gccgtgcca aacgcaacgtc gacatcctca gggacttctg tgcggagcag aacatcaagt 540  
 acttctatga catcaaggac ctccagcgatt tcagggtctaa tccggactac aaaggcgtct 600  
 gccacatcgc acttgctcag gaagcccact gccgaccagg cgaggttctc ttgggcactg 660  
 attctcatac atgcaatgct ggagcttttg gtcagtttgc aactggaatc ggaaacactg 720  
 atgcaggttt tgtgttgggc actggaaagg ctcttctcaa ggtgccacct actatcaggt 780  
 ttatattaga tggagagatg ccgccttatt tacttgcgaa ggatctgatt ttgcaaatta 840  
 ttggagagat ttcagtatct ggtgcgacct acaaatcaat ggagtttgtt ggatcaactg 900  
 tagaagctct aacctggaa gagcgtatga cactatgcaa catggttatt gaagctgggtg 960  
 gaaagaacgg tgttgtgcct gctgatgaaa ctacatttaa ataccttgag ggtaagacat 1020  
 cagtcgatta tgaacctgtc tacagtgatg ctcaagccag attttttagc gactaccggt 1080  
 ttgatgtatc aaaactggag ccagtgttg ccaagccaca ttgcctgac aaccgtgctc 1140  
 cagcaacgga atgcaaagat gtgaagatcg accgagtcta tattggttct tgcaactggtg 1200  
 gtaagaccga ggatttcctt gctgtgcaa aggtgttctt agcctcgga agaaggtta 1260  
 aagttccac atttcttgtc cctgccacac aaaaggtgtg gttggacata tatagcctcc 1320  
 ctgtaccagg atctggtggc aaaacttgct ccagatatt tgaggaggct gggtgtgaca 1380

caccagcaag tcctaattgt ggtgcttgtt tgggtggccc tcgtgataca tatgcacgga 1440  
tgaatgaacc tactgtctgc gtgtccacca cgaacaggaa ctttcgggc aggatgggcc 1500  
acaaggaagg gcaaattctac ctggcgtctc cctacactgc ggctgcctca gccctgacgg 1560  
ggtatgttac ggaccccaag gacttcctca tgaaccgtc ttgaaacaac aacagatttc 1620  
atgatgtaac agagtgggtg tactgtctgt tttcgtgctg aacttttgtc cangcatgtc 1680  
cttcgttg 1688

<210> 38  
<211> 443  
<212> PRT  
<213> Zea mays

<400> 38  
Met Thr Met Thr Glu Lys Ile Leu Ala Arg Ala Ser Glu Arg Ala Ala  
1 5 10 15

Leu Glu Pro Gly Glu Asn Val Trp Val Asp Val Asp Val Leu Met Thr  
20 25 30

His Asp Val Cys Gly Pro Gly Ala Phe Asp Ile Phe Lys Lys Glu Phe  
35 40 45

Gly Glu Asp Ala Arg Val Trp Asp Arg Glu Lys Leu Val Val Ile Pro  
50 55 60

Asp His Tyr Ile Phe Thr Ser Asp Gly Arg Ala Lys Arg Asn Val Asp  
65 70 75 80

Ile Leu Arg Asp Phe Cys Ala Glu Gln Asn Ile Lys Tyr Phe Tyr Asp  
85 90 95

Ile Lys Asp Leu Ser Asp Phe Arg Ala Asn Pro Asp Tyr Lys Gly Val  
100 105 110

Cys His Ile Ala Leu Ala Gln Glu Ala His Cys Arg Pro Gly Glu Val  
115 120 125

Leu Leu Gly Thr Asp Ser His Thr Cys Asn Ala Gly Ala Phe Gly Gln  
130 135 140

Phe Ala Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Leu Gly Thr  
145 150 155 160

Gly Lys Ala Leu Leu Lys Val Pro Pro Thr Ile Arg Phe Ile Leu Asp  
165 170 175

Gly Glu Met Pro Pro Tyr Leu Leu Ala Lys Asp Leu Ile Leu Gln Ile  
180 185 190

Ile Gly Glu Ile Ser Val Ser Gly Ala Thr Tyr Lys Ser Met Glu Phe  
195 200 205

Val Gly Ser Thr Val Glu Ser Leu Thr Met Glu Glu Arg Met Thr Leu  
210 215 220

Cys Asn Met Val Ile Glu Ala Gly Gly Lys Asn Gly Val Val Pro Ala  
225 230 235 240

Asp Glu Thr Thr Phe Lys Tyr Leu Glu Gly Lys Thr Ser Val Asp Tyr  
245 250 255

Glu Pro Val Tyr Ser Asp Ala Gln Ala Arg Phe Phe Ser Asp Tyr Arg  
260 265 270

Phe Asp Val Ser Lys Leu Glu Pro Val Val Ala Lys Pro His Ser Pro  
275 280 285

Asp Asn Arg Ala Pro Ala Arg Glu Cys Lys Asp Val Lys Ile Asp Arg  
 290 295 300  
 Val Tyr Ile Gly Ser Cys Thr Gly Gly Lys Thr Glu Asp Phe Leu Ala  
 305 310 315 320  
 Ala Ala Lys Val Phe Leu Ala Ser Gly Lys Lys Val Lys Val Pro Thr  
 325 330 335  
 Phe Leu Val Pro Ala Thr Gln Lys Val Trp Leu Asp Ile Tyr Ser Leu  
 340 345 350  
 Pro Val Pro Gly Ser Gly Gly Lys Thr Cys Ser Gln Ile Phe Glu Glu  
 355 360 365  
 Ala Gly Cys Asp Thr Pro Ala Ser Pro Asn Cys Gly Ala Cys Leu Gly  
 370 375 380  
 Gly Pro Arg Asp Thr Tyr Ala Arg Met Asn Glu Pro Thr Val Cys Val  
 385 390 395 400  
 Ser Thr Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly  
 405 410 415  
 Gln Ile Tyr Leu Ala Ser Pro Tyr Thr Ala Ala Ala Ser Ala Leu Thr  
 420 425 430  
 Gly Tyr Val Thr Asp Pro Lys Asp Phe Leu Met  
 435 440

<210> 39  
 <211> 512  
 <212> DNA  
 <213> Oryza sativa

<220>  
 <221> unsure  
 <222> (303)..(303)

<220>  
 <221> unsure  
 <222> (331)

<220>  
 <221> unsure  
 <222> (400)

<220>  
 <221> unsure  
 <222> (467)

<220>  
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 <222> (486)

<220>  
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 <222> (495)

<220>  
 <221> unsure  
 <222> (509)

<400> 39  
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 cttggtactg atttctatac atgcaatgct ggagcctttg gccaatattgc aactgggaatt 120  
 ggaaacactg atgctgggtt tgtgatgggc actgggaagg ctcttcttaa ggtgcctcca 180  
 actatcaggt ttgtattaga tggagaaatg ccaccttatt tacttgcaaa ggatctgatt 240  
 ttacaaatta ttggtgagat ttctgtatct ggcgcaacat acaaatccat ggagtttgtt 300  
 ggntcaactg tggaaagtct aaatatggaa nagcgaatga cactgtgcaa catggttatt 360  
 gaagctggtg gcaagaatgg tgttgtgcct gcccgatcan actacattta actatcttga 420  
 gggcaagaca tcagttgaat acgagcctgt catagtgatg ctcaagncaa atttgtagt 480  
 gactancggt ttgangtata caaatggng ca 512

<210> 40  
 <211> 127  
 <212> PRT  
 <213> *Oryza sativa*

<220>  
 <221> UNSURE  
 <222> (109)

<400> 40  
 Val Cys His Val Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly Glu  
 1 5 10 15  
 Val Leu Leu Gly Thr Asp Ser His Thr Cys Asn Ala Gly Ala Phe Gly  
 20 25 30  
 Gln Phe Ala Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Met Gly  
 35 40 45  
 Thr Gly Lys Ala Leu Leu Lys Val Pro Pro Thr Ile Arg Phe Val Leu  
 50 55 60  
 Asp Gly Glu Met Pro Pro Tyr Leu Leu Ala Lys Asp Leu Ile Leu Gln  
 65 70 75 80  
 Ile Ile Gly Glu Ile Ser Val Ser Gly Ala Thr Tyr Lys Ser Met Glu  
 85 90 95  
 Phe Val Gly Ser Thr Val Glu Ser Leu Asn Met Glu Xaa Arg Met Thr  
 100 105 110  
 Leu Cys Asn Met Val Ile Glu Ala Gly Gly Lys Asn Gly Val Val  
 115 120 125

<210> 41  
 <211> 823  
 <212> DNA  
 <213> Glycine max

<400> 41  
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 ctcgcagagt atagatttga tgtctcaaaa ttggagccag tgggtggccaa gcctcattct 120  
 ccggataatc gtgcttttggc aagagagtgc aaggatgtga aaattgacag agtatacata 180  
 ggatcttgta caggtggcaa aacagaggat ttcattggctg cagcaaaaagt ttttctggca 240  
 tcaggtaaac aggtcaaagt tcctacattt cttgtgcytg caacacaaaa ggtttggatg 300  
 gacttgtaact ccctccctgt ccctggatct ggtggtaaga catgctcaca gatatttgaa 360  
 gaagttgggt gtgacacacc agctagtcct agttgtgggt cttgtttggg tggcccaaaa 420  
 gatacttacg cagcatgaa tgaacctaa gtttgtgtt caactacgaa caggaaacttc 480  
 ccgggccgaa tgggacacaa ggaaggtcaa atctatttgg cttcccctta tacagctgct 540  
 gcatctgcat tgaccggtta tgttactgat cctagagagt tctttagta gaatgttgtt 600  
 acaatcatct cattgtgttg tactcgttgt tggttatttg tgtattctct actctctact 660  
 agtcataagt taaaactgac aactatttaa gcttaaccaa tcttttagta tttctaagtt 720  
 gatctttaga atcattcata tatgtgggtt aggtcaattc agatcaacat gaagttcaat 780  
 ttcaaattha gtagtgtttg gtctttttaa aaaaaaaaaaaa aaa 823

<210> 42  
 <211> 195  
 <212> PRT  
 <213> Glycine max

<220>  
 <221> UNSURE  
 <222> (93)

<400> 42  
 Leu Glu Gly Lys Thr Ser Leu Pro Tyr Glu Pro Val Tyr Ser Asp Asp  
 1 5 10 15  
 Gln Ala Arg Phe Leu Ala Glu Tyr Arg Phe Asp Val Ser Lys Leu Glu  
 20 25 30  
 Pro Val Val Ala Lys Pro His Ser Pro Asp Asn Arg Ala Leu Ala Arg  
 35 40 45  
 Glu Cys Lys Asp Val Lys Ile Asp Arg Val Tyr Ile Gly Ser Cys Thr  
 50 55 60  
 Gly Gly Lys Thr Glu Asp Phe Met Ala Ala Ala Lys Val Phe Leu Ala  
 65 70 75 80  
 Ser Gly Lys Gln Val Lys Val Pro Thr Phe Leu Val Xaa Ala Thr Gln  
 85 90 95  
 Lys Val Trp Met Asp Leu Tyr Ser Leu Pro Val Pro Gly Ser Gly Gly  
 100 105 110  
 Lys Thr Cys Ser Gln Ile Phe Glu Glu Val Gly Cys Asp Thr Pro Ala  
 115 120 125  
 Ser Pro Ser Cys Gly Ala Cys Leu Gly Gly Pro Lys Asp Thr Tyr Ala  
 130 135 140  
 Arg Met Asn Glu Pro Lys Val Cys Val Ser Thr Thr Asn Arg Asn Phe  
 145 150 155 160  
 Pro Gly Arg Met Gly His Lys Glu Gly Gln Ile Tyr Leu Ala Ser Pro  
 165 170 175  
 Tyr Thr Ala Ala Ala Ser Ala Leu Thr Gly Tyr Val Thr Asp Pro Arg  
 180 185 190

Glu Phe Leu  
 195

<210> 43  
 <211> 530  
 <212> DNA  
 <213> Triticum aestivum

<400> 43  
 gcacgagctt tattgctgct gcaaaggtgt tottagcttc gggcaagaag gttaagggttc 60  
 ccacttttct cgttcctgcg actcaaaagg tgtggatgga cgtgtatagt ctccccgtac 120  
 caggatctgg tggcaaaaca tgctcccaga tatttgaaga ggctgggttg gatacaccag 180  
 ctagtccctaa ttgtggtgct tgtttggtg gtctcgtga tacatatgca cggatgaatg 240  
 aacctacggt ctgtgtatca acgacgaaca ggaacttccc gggcaggatg ggccacaagg 300  
 aagggcagat ctacctggct tctcccttca ccgcggcggc ctcagctttg acgggatatg 360  
 tcacggaccc cagggacttc ctgtcgtaga gatcttgaaa acaatgaatt tgtgttgcg 420  
 accgtcctgt actggtactt tttgttcgtg ttcgaaactg tagtttagat gcgtcatgtg 480  
 tgtgtcgtgc tgagaaataa gctactcaac gagtagcagt tgtaactgtt 530



<210> 44  
 <211> 126  
 <212> PRT  
 <213> Triticum aestivum

<400> 44  
 Phe Ile Ala Ala Ala Lys Val Phe Leu Ala Ser Gly Lys Lys Val Lys  
 1 5 10 15  
 Val Pro Thr Phe Leu Val Pro Ala Thr Gln Lys Val Trp Met Asp Val  
 20 25 30  
 Tyr Ser Leu Pro Val Pro Gly Ser Gly Gly Lys Thr Cys Ser Gln Ile  
 35 40 45  
 Phe Glu Glu Ala Gly Cys Asp Thr Pro Ala Ser Pro Asn Cys Gly Ala  
 50 55 60  
 Cys Leu Gly Gly Pro Arg Asp Thr Tyr Ala Arg Met Asn Glu Pro Thr  
 65 70 75 80  
 Val Cys Val Ser Thr Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His  
 85 90 95  
 Lys Glu Gly Gln Ile Tyr Leu Ala Ser Pro Phe Thr Ala Ala Ala Ser  
 100 105 110  
 Ala Leu Thr Gly Tyr Val Thr Asp Pro Arg Asp Phe Leu Ser  
 115 120 125

<210> 45  
 <211> 424  
 <212> PRT  
 <213> Methanococcus jannaschii

<400> 45  
 Met Gly Met Thr Ile Val Glu Lys Ile Leu Ala Lys Ala Ser Gly Lys  
 1 5 10 15  
 Lys Glu Val Ser Pro Gly Asp Ile Val Met Ala Asn Ile Asp Val Ala  
 20 25 30  
 Met Val His Asp Ile Thr Gly Pro Leu Thr Val Asn Thr Leu Lys Glu  
 35 40 45  
 Tyr Gly Ile Glu Lys Val Trp Asn Pro Glu Lys Ile Val Ile Leu Phe  
 50 55 60  
 Asp His Gln Val Pro Ala Asp Ser Ile Lys Ala Ala Glu Asn His Ile  
 65 70 75 80  
 Leu Met Arg Lys Phe Val Lys Glu Gln Gly Ile Lys Tyr Phe Tyr Asp  
 85 90 95  
 Ile Arg Glu Gly Val Cys His Gln Val Leu Pro Glu Lys Gly His Val  
 100 105 110  
 Ala Pro Gly Glu Val Val Val Gly Ala Asp Ser His Thr Cys Thr His  
 115 120 125  
 Gly Ala Phe Gly Ala Phe Ala Thr Gly Ile Gly Ser Thr Asp Met Ala  
 130 135 140  
 His Val Phe Ala Thr Gly Lys Leu Trp Phe Lys Val Pro Glu Thr Ile  
 145 150 155 160

Tyr Phe Asn Ile Thr Gly Asp Leu Gln Pro Tyr Val Thr Ser Lys Asp  
 165 170 175  
 Val Ile Leu Ser Ile Ile Gly Glu Val Gly Val Asp Gly Ala Thr Tyr  
 180 185 190  
 Lys Ala Cys Gln Phe Gly Gly Glu Thr Val Lys Lys Met Ser Ile Ala  
 195 200 205  
 Ser Arg Met Thr Met Thr Asn Met Ala Ile Glu Met Gly Gly Lys Thr  
 210 215 220  
 Gly Ile Ile Glu Pro Asp Glu Lys Thr Ile Gln Tyr Val Lys Glu Ala  
 225 230 235 240  
 Met Lys Lys His Gly Thr Glu Arg Pro Phe Glu Val Ile Lys Gly Asp  
 245 250 255  
 Glu Asp Ala Glu Phe Ala Glu Val Tyr Glu Ile Glu Ala Asp Lys Ile  
 260 265 270  
 Glu Pro Val Phe Ala Cys Pro His Asn Val Asp Asn Val Lys Gln Ala  
 275 280 285  
 Arg Glu Val Ala Gly Lys Pro Ile Asp Gln Val Phe Ile Gly Ser Cys  
 290 295 300  
 Thr Asn Gly Arg Leu Glu Asp Leu Arg Met Ala Ile Lys Ile Ile Glu  
 305 310 315 320  
 Lys His Gly Gly Ile Ala Asp Asp Val Arg Val Val Val Thr Pro Ala  
 325 330 335  
 Ser Arg Glu Glu Tyr Leu Lys Ala Leu Lys Glu Gly Ile Ile Glu Lys  
 340 345 350  
 Phe Leu Lys Tyr Gly Cys Val Val Thr Asn Pro Ser Cys Ser Ala Cys  
 355 360 365  
 Met Gly Ser Leu Tyr Gly Val Leu Gly Pro Gly Glu Val Cys Val Ser  
 370 375 380  
 Thr Ser Asn Arg Asn Phe Arg Gly Arg Gln Gly Ser Leu Glu Ala Glu  
 385 390 395 400  
 Ile Tyr Leu Ala Ser Pro Ile Thr Ala Ala Cys Ala Val Lys Gly  
 405 410 415  
 Glu Leu Val Asp Pro Arg Asp Leu  
 420

<210> 46  
 <211> 1033  
 <212> DNA  
 <213> Zea mays

<400> 46  
 atcatggcgg cggtctgtgc ggggacggcg gtgtccacgg cagcgcttct agccccaatc 60  
 cgagctccaa ccagcgcgtt tatccggcgc tcccagctca cctgtcatcg cctccactca 120  
 ctaaaatgcc gcgcgcgtgg gtccatcgtc cccgcggccg ctgctgccgc ggcggggcagc 180  
 agctcgccgt cgtcagccgt tttccacggc gactgcttcg tgggtgggca caatatcgac 240  
 accgaccaga tcatccccgc cgagcacctc actctgggtgc cctccaagcc ggacgagtac 300  
 cgcaagctcg gttccttcgc cttcgcgggg ctcccatccg cggcctaccc gacgccgttc 360  
 gtcgctccgg gtgaggagtc ctcccgtac gccatcattg tcggcggagc caacttcggg 420  
 tgcggttctt ctgcgcagca cgcgcccgtc gcgcttgagg ccgctggcgc acgcgccatt 480  
 gttgcsagag gctacgcgcg catctttttt cgcaactccg tggccactgg agaggtgtac 540

```

cctctggagc tcaacggacgt tggggcctgg aaggagtgc agacagggga tgtggtcacc 600
gtggaccttg ctaactccgt ttttattaac cacacctctg gcaaggagta caagctgaaa 660
ccaattggtg atgctggccc tgtaattgag gcgggaggga tctttgccta cgcccggaag 720
acaggaatga ttgcgtcgaa agctgctgca tgagggaag cttatgcagc cgagcctctg 780
cggagatgaa gaagtaagct ggagttagga ctaagagtta ctgcacctac ttgatgtcga 840
cgggtgtctca aaataagttg cggcctaccg aaattatgat gaatcaatca atttggtctt 900
tgtcacagat cgtttttttt tgttactagt acttgtacaa ttgtactcct gcctgctact 960
gttcttatct gtttgaataa ctgctctgtt gccaaaaaaa aaaaaaaaaa aaaaaaaaaa 1020
aaaaaaaaaa aaa                                     1033

```

```

<210> 47
<211> 249
<212> PRT
<213> Zea mays

```

<400> 47

```

Met Ala Ala Ala Leu Ser Gly Thr Ala Val Ser Thr Ala Ala Leu Leu
  1             5             10             15

```

```

Ala Pro Ile Arg Ala Pro Thr Ser Ala Phe Ile Arg Arg Ser Gln Leu
          20             25             30

```

```

Thr Cys His Arg Leu His Ser Leu Lys Cys Arg Arg Ala Gly Ser Ile
          35             40             45

```

```

Val Pro Ala Ala Ala Ala Ala Ala Gly Ser Ser Ser Pro Ser Ser
          50             55             60

```

```

Ala Val Phe His Gly Glu Cys Phe Val Val Gly Asp Asn Ile Asp Thr
          65             70             75             80

```

```

Asp Gln Ile Ile Pro Ala Glu His Leu Thr Leu Val Pro Ser Lys Pro
          85             90             95

```

```

Asp Glu Tyr Arg Lys Leu Gly Ser Phe Ala Phe Ala Gly Leu Pro Ser
          100            105            110

```

```

Ala Ala Tyr Pro Thr Pro Phe Val Ala Pro Gly Glu Glu Ser Ser Arg
          115            120            125

```

```

Tyr Ala Ile Ile Val Gly Gly Ala Asn Phe Gly Cys Gly Ser Ser Arg
          130            135            140

```

```

Glu His Ala Pro Val Ala Leu Gly Ala Ala Gly Ala Arg Ala Ile Val
          145            150            155            160

```

```

Ala Glu Gly Tyr Ala Arg Ile Phe Phe Arg Asn Ser Val Ala Thr Gly
          165            170            175

```

```

Glu Val Tyr Pro Leu Glu Leu Thr Asp Val Gly Ala Trp Lys Glu Cys
          180            185            190

```

```

Lys Thr Gly Asp Val Val Thr Val Asp Leu Ala Asn Ser Val Phe Ile
          195            200            205

```

```

Asn His Thr Ser Gly Lys Glu Tyr Lys Leu Lys Pro Ile Gly Asp Ala
          210            215            220

```

```

Gly Pro Val Ile Glu Ala Gly Gly Ile Phe Ala Tyr Ala Arg Lys Thr
          225            230            235            240

```

```

Gly Met Ile Ala Ser Lys Ala Ala Ala
          245

```

```

<210> 48
<211> 1112

```

<212> DNA  
<213> Oryza sativa

<400> 48  
gaagtgggttc tccctcacac actgaacacc atggcggcgg cggcggcggc tccgggtcta 60  
tccttgggccg aggcggcgcc ggtgacagca gttctggcac cgtgtccac gccctcgagg 120  
acgttccgcc gccgcagctg ggtcgcggct atctgccggc ccgccctgaa atgccaccac 180  
agtcgtcccc tgaccgccgt ggtcgcggcg gctgcggctg ccgctgcggc gggggactcg 240  
acgtcggccg gcgtattcca cggcgagtgc ttcgtcgtgg gggataacat cgacaccgac 300  
cagatcatcc cggccgagca cctgaccctg gtcccgcca agcccgacga gtaccgcaag 360  
ctcggctcgt tcgccttcgt cggcctcccc accgcggcct acccgacgcc gttcgtcgcc 420  
cccggcgagg agaccacccg ctacgcgcgc atcatcggcg gcgccaactt cggctgcggc 480  
tcctcccgcg agcacgcgcc cgtcgccttg ggccgcggc gcgcccgcc cgtcgtggcc 540  
gagggctacg cgcgcattct cttccgcaac tccgtggcca ccggtgaggt ctaccggttg 600  
gagctagcgg acactggagc ctggaaggag tgcaagaccg gggatgtggt cacggtggaa 660  
cttgataatt gcgtcatgat caaccacaca tccggcaagc agtacaagct gaagcctatc 720  
ggcgatgccg ggccggttat tgaggcaggc gggatctttg cctatgcccg gaagaccgga 780  
atgatcgcat ccaagtctgc gtgagggaaa ggcgagtttg gtctgctgtc aagatagtcg 840  
aggcctctgc agatagcaag taagactggg ttgtggattt gaacctattg cacctctatg 900  
cgattgtcca tcagttgtac tgctgttttt acctaggttg tgtgtcatca gtggtgtttt 960  
tggaataagt taaaagttac agagtactga actatgatgt attagtccat gtgatcttat 1020  
gtaacacctt atgtaataca ctcgtttata cctgccgatt tgcctatctc gtttcgataa 1080  
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1112

<210> 49  
<211> 257  
<212> PRT  
<213> Oryza sativa

<400> 49  
Met Ala Ala Ala Ala Ala Pro Ala Leu Ser Leu Ala Glu Ala Ala  
1 5 10 15  
Pro Val Thr Ala Val Leu Ala Pro Cys Pro Thr Pro Ser Arg Thr Phe  
20 25 30  
Arg Arg Arg Ser Trp Val Ala Ala Ile Cys Arg Pro Ala Leu Lys Cys  
35 40 45  
His His Ser Arg Pro Leu Thr Ala Val Val Ala Ala Ala Ala Ala Ala  
50 55 60  
Ala Ala Ala Gly Asp Ser Thr Ser Ala Gly Val Phe His Gly Glu Cys  
65 70 75 80  
Phe Val Val Gly Asp Asn Ile Asp Thr Asp Gln Ile Ile Pro Ala Glu  
85 90 95  
His Leu Thr Leu Val Pro Ser Lys Pro Asp Glu Tyr Arg Lys Leu Gly  
100 105 110  
Ser Phe Ala Phe Val Gly Leu Pro Thr Ala Ala Tyr Pro Thr Pro Phe  
115 120 125  
Val Ala Pro Gly Glu Glu Thr Thr Arg Tyr Ala Val Ile Ile Gly Gly  
130 135 140  
Ala Asn Phe Gly Cys Gly Ser Ser Arg Glu His Ala Pro Val Ala Leu  
145 150 155 160  
Gly Ala Ala Gly Ala Arg Ala Val Val Ala Glu Gly Tyr Ala Arg Ile  
165 170 175  
Phe Phe Arg Asn Ser Val Ala Thr Gly Glu Val Tyr Pro Leu Glu Leu  
180 185 190

Ala Asp Thr Gly Ala Trp Lys Glu Cys Lys Thr Gly Asp Val Val Thr  
195 200 205

Val Glu Leu Asp Asn Cys Val Met Ile Asn His Thr Ser Gly Lys Gln  
210 215 220

Tyr Lys Leu Lys Pro Ile Gly Asp Ala Gly Pro Val Ile Glu Ala Gly  
225 230 235 240

Gly Ile Phe Ala Tyr Ala Arg Lys Thr Gly Met Ile Ala Ser Lys Ser  
245 250 255

Ala

<210> 50  
<211> 1107  
<212> DNA  
<213> Glycine max

<400> 50  
tggaaatgag aaaatagacg gaagtgagag aggaggcact gagcatccaa caatggcctt 60  
gcacgagggt ctcttctgcc gcaaccgttc ttctogggaa cctggcattc accaaactct 120  
ccctctctca ctctcacact cttctaccgc gcttctcttc tttcccaact cccaagtcac 180  
caaaccctcg caaccgcgtc gcagtctctc tccaaacccc acgcgctcaa tccgccgcgt 240  
ccgcttctcc ctccgcctcc ttccaaggcc tctgctacgt cgtcggcgac aatatcgaca 300  
ccgaccagat cattcccgcc gactacctca ccctcgctcc ttccaagccc gacgagtacg 360  
agaagctcgg ctctacgcc ctcatcgcc tccccgccac ctacgccacg cgtttcatcg 420  
aaccggcgga gatcaaaaac aagtagccca tgcgtatcgg cggtgccaac ttcggttgcg 480  
gctcctcccg cgagcacgcc ccgctcgccg tgggcgcctc cggcgccgcc gcagtggctg 540  
cggagtcgta cgctaggatc ttctttcgga actccgtggc caccggcgag gtgtatccgc 600  
tagagtcgga gggacgcctc tgcgaggagt gcaccaccgg cgatgtggtg acgattgagc 660  
tcggagagag ccgcttgatc aatcacacca ccggaaagga gtatcgcttg aaaccgatcg 720  
gogacggggg tccagtgatc gaggccgggtg gcattcttgc ctatgccagg aaaaccggca 780  
tgattccctc tcggttgagtt cttcaggtga gggcagtgaa ctctgctatc cttgcttcag 840  
atgacatgct tctcaagaaa tgtattgacc caatggatgc cttagcttgg tccattatca 900  
aataggctag aacttgcaga gatataatag atggcaatag aaagtgtgtt ttaatggttc 960  
ttgcatcagc agcttctttt ataattctcat tgatatggg tatctcatta atgcaaactt 1020  
ttgtattcac gaaatgggac caattttgcc ccatttatca atcagaatgg tacttatttt 1080  
tcctcgggca aaaaaaaaaa aaaaaag 1107

<210> 51  
<211> 263  
<212> PRT  
<213> Glycine max

<220>  
<221> UNSURE  
<222> (4)

<400> 51  
Met Arg Lys Xaa Thr Glu Val Arg Glu Glu Ala Leu Ser Ile Gln Gln  
1 5 10 15

Trp Pro Cys Thr Arg Phe Ser Ser Ala Ala Thr Val Leu Pro Arg Asn  
20 25 30

Leu Ala Phe Thr Lys Leu Ser Leu Ser His Ser His Thr Leu Leu Pro  
35 40 45

Arg Phe Leu Ser Phe Pro Thr Pro Lys Ser Ser Asn Pro Arg Asn Arg  
50 55 60

Val Ala Val Ser Leu Gln Thr Pro Arg Ala Gln Ser Ala Ala Ser Ala  
65 70 75 80

Ser Pro Ser Ala Ser Phe His Gly Leu Cys Tyr Val Val Gly Asp Asn  
85 90 95

Ile Asp Thr Asp Gln Ile Ile Pro Ala Glu Tyr Leu Thr Leu Val Pro  
100 105 110

Ser Lys Pro Asp Glu Tyr Glu Lys Leu Gly Ser Tyr Ala Leu Ile Gly  
115 120 125

Leu Pro Ala Thr Tyr Ala Thr Arg Phe Ile Glu Pro Gly Glu Ile Lys  
130 135 140

Thr Lys Tyr Ala Ile Val Ile Gly Gly Ala Asn Phe Gly Cys Gly Ser  
145 150 155 160

Ser Arg Glu His Ala Pro Val Ala Leu Gly Ala Ser Gly Ala Ala Ala  
165 170 175

Val Val Ala Glu Ser Tyr Ala Arg Ile Phe Phe Arg Asn Ser Val Ala  
180 185 190

Thr Gly Glu Val Tyr Pro Leu Glu Ser Glu Gly Arg Leu Cys Glu Glu  
195 200 205

Cys Thr Thr Gly Asp Val Val Thr Ile Glu Leu Gly Glu Ser Arg Leu  
210 215 220

Ile Asn His Thr Thr Gly Lys Glu Tyr Arg Leu Lys Pro Ile Gly Asp  
225 230 235 240

Ala Gly Pro Val Ile Glu Ala Gly Gly Ile Phe Ala Tyr Ala Arg Lys  
245 250 255

Thr Gly Met Ile Pro Ser Arg  
260

<210> 52  
<211> 995  
<212> DNA  
<213> Triticum aestivum

<400> 52  
gcacgagcgg cgggtgtccac ggcagcgcgtt ctagccccc aa tccgagctcc aaccagcgcg 60  
tttatccggc gctcccagct cacctgtcat cgcctccact cactaaaatg ccgcccgcgt 120  
gggtccatcg tccccgcggc cgctgtgcc gcggcgggca gcagctcgcc gtcgtcagcc 180  
gttttccacg gcgagtgtt cgtgggtggc gacaatatcg acaccgacca gatcatcccc 240  
gccgagcacc tcaactctgt gccctccaag ccgacgagc accgcaagct cggttccttc 300  
gccttcgcgg ggctcccatc cgcggcctac ccgacgccgt tcgtcgtcc gggtgaggag 360  
tcctcccgt acgccatcat tgtcggcgga gccaaactcg ggtgcggttc ctctcgcgag 420  
cacgcgcccg tcgcgcttgg ggccgctggc gcacgcgcca ttgttgcgga gggctacgcg 480  
cgcattcttt ttcgcaactc cgtgggcact ggagaggtgt accctctgga gctcacggac 540  
gttggggcct ggaaggagt caagacagg gatgtggtca ccgtggacct tgctaactcc 600  
gtttttatta accacacctc tggcaaggag tacaagctga aaccaattgg tgatgctggc 660  
cctgtaattg aggcgggagg gatctttgcc tacgcccgga agacaggaat gattgcgtcg 720  
aaagctgctg catgaggaa agatcagct atgcagccga gcctctgcgg agatgaagaa 780  
gtaagctgga gttaggacta agagtactg cacctacttg atgtcgacgg tgtctcaaaa 840  
taagttgcgg cctaccgaaa ttatgatgaa tcaatcaatt tggctttgt cacagatcgt 900  
tttttttgt tactagtact tgtacaattg tactcctgcc tgctactgtt cttatctgtt 960  
tgaataactg ctctgttgcc atctaaaaaa aaaaa 995

<210> 53  
<211> 244  
<212> PRT  
<213> Triticum aestivum

<400> 53  
Ala Arg Ala Ala Val Ser Thr Ala Ala Leu Leu Ala Pro Ile Arg Ala  
1 5 10 15  
Pro Thr Ser Ala Phe Ile Arg Arg Ser Gln Leu Thr Cys His Arg Leu  
20 25 30  
His Ser Leu Lys Cys Arg Arg Ala Gly Ser Ile Val Pro Ala Ala Ala  
35 40 45  
Ala Ala Ala Ala Gly Ser Ser Ser Pro Ser Ser Ala Val Phe His Gly  
50 55 60  
Glu Cys Phe Val Val Gly Asp Asn Ile Asp Thr Asp Gln Ile Ile Pro  
65 70 75 80  
Ala Glu His Leu Thr Leu Val Pro Ser Lys Pro Asp Glu Tyr Arg Lys  
85 90 95  
Leu Gly Ser Phe Ala Phe Ala Gly Leu Pro Ser Ala Ala Tyr Pro Thr  
100 105 110  
Pro Phe Val Ala Pro Gly Glu Glu Ser Ser Arg Tyr Ala Ile Ile Val  
115 120 125  
Gly Gly Ala Asn Phe Gly Cys Gly Ser Ser Arg Glu His Ala Pro Val  
130 135 140  
Ala Leu Gly Ala Ala Gly Ala Arg Ala Ile Val Ala Glu Gly Tyr Ala  
145 150 155 160  
Arg Ile Phe Phe Arg Asn Ser Val Gly Thr Gly Glu Val Tyr Pro Leu  
165 170 175  
Glu Leu Thr Asp Val Gly Ala Trp Lys Glu Cys Lys Thr Gly Asp Val  
180 185 190  
Val Thr Val Asp Leu Ala Asn Ser Val Phe Ile Asn His Thr Ser Gly  
195 200 205  
Lys Glu Tyr Lys Leu Lys Pro Ile Gly Asp Ala Gly Pro Val Ile Glu  
210 215 220  
Ala Gly Gly Ile Phe Ala Tyr Ala Arg Lys Thr Gly Met Ile Ala Ser  
225 230 235 240  
Lys Ala Ala Ala

<210> 54  
<211> 113  
<212> PRT  
<213> Lactococcus lactis

<400> 54  
Met Lys Thr Tyr Lys Gly Thr Ser Val Val Met Asn Asp Asn Asp Thr  
1 5 10 15  
Asp Lys Lys Ala Asp Lys Lys Gly Gly Lys Asn Tyr Trp Arg Tyr Lys  
20 25 30  
Asp Tyr Asp Asn Asp Asn Ala Lys Tyr Lys Lys Ala Ser Ser Gly Asp  
35 40 45  
Asn Gly Ser Gly Ser Ser Arg His Ala Ala Trp Ala Ser Asp Tyr Gly  
50 55 60

Arg	Ala	Ala	Gly	Ser	Tyr	Ser	Asp	Tyr	Asn	Asn	Ala	Lys	Asn	Gly	Lys
65					70					75					80
Arg	Val	Asn	Thr	Lys	Ser	Ser	Thr	Asp	His	Thr	Ser	Gly	Asp	His	Asp
				85					90					95	
Trp	Lys	Asp	Lys	Asn	Gly	Asp	Asp	Gly	Thr	Tyr	Ala	Ser	Ala	Tyr	Lys
			100					105					110		

Asn